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7, 2003, 03:15:26 ; Search time 101 Seconds (without alignments) 5902.769 Million cell updates/sec
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Minimum DB seq length: 0
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Maximum Match 100%
Listing first 45 summaries

Database: Issued\_Patents\_NA:\*

1: \cgn2\_6/\text{ptodata}/1/\ina/5A\_COMB.seq:\*

2: \cgn2\_6/\text{ptodata}/1/\ina/5B\_COMB.seq:\*

3: \cgn2\_6/\text{ptodata}/1/\ina/6A\_COMB.seq:\*

4: \cgn2\_6/\text{ptodata}/1/\ina/6A\_COMB.seq:\*

5: \cgn2\_6/\text{ptodata}/1/\ina/6B\_COMB.seq:\*

6: \cgn2\_6/\text{ptodata}/1/\ina/PCTUS\_COMB.seq:\*

6: \cgn2\_6/\text{ptodata}/1/\ina/PCTUS\_COMB.seq:\*

6: \cgn2\_6/\text{ptodata}/1/\ina/PacKfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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	Description	Sequence 4, Appli	ď	7	Sequence 1, Appli	Ĥ	o,	Ĥ	24,	4, 2	H	Sequence 10, Appl	4		17			ď	7	ને	ત્તે	'n	Н	15,	15,	15,	Η	15,
SUMMARIES	E	US-C9-228-986-4	US-09-228-986-9	-228-986-	-265	-881	US-07-717-331F-9	US-07-717-331F-1	-587	-717	US-09-228-986-1	US-09-228-986-10	US-08-447-185-2	US-08-447-185-3	US-09-228-986-11	GS-08-781-891-208	US-09-249-585A-2	US-09-050-863-2	US-09-359-081-2	US-09-130-114-1	ęΓ	US-09-620-925-1	-884-	US-07-885-971-15	US-08-087-783A-15	88	US-08-194-087-15	PCT-DS93-04648-15
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	Query Match Length	28	$^{\prime\prime}$	2432	2749	5	2571	2833	1554	2749	2389	2336	996	2443	3097	16442	1926	2580	2580	5452	0096	0096	10595	10596	10596	10596	10596	10596
de	Query	9.4	9.2	9.0	8.6	8.4		7.5	7.2	7.2	7.1	6.7	6.2	6.2	6.1	6.1	ο.	ي. د.	5.9	5,9	5.9	5.9	5.9	5, 0	5.9	υ,	5.9	ر. و
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US-09-503-922-2	US-08-232-463-14	US-08-781-891-209	US-08-473-553A-1	US-07-915-246-1	US-09-228-986-12	US-08-217-327-3	US-07-885-970A-3	US-08-298-687A-3	US-08-530-797-2	US-08-298-829-3	US-08-787-335-2	US-07-885-970A-25	US-08-298-687A-25	US-08-298-829-25	US-08-728-323A-1	US-09-298-568-I	US-03-770-379-20	
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## ALIGNMENTS

US-09-228-986-4

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Sequence 4, Application US/09228986
Fatent No. 6355198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Compositions in the Modification of Plant Cell Signalling
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DAIE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 8.9e-36;
0; Mismatches 400; Indels
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Best Local Similarity 52.9%;
Matches 467; Conservative (
                                                                                                                                                                                                                                                                     ) TYPE: DNA
) ORGANISM: Pinus radiata
US-09-228-936-4
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Sequence 7, Application US/09223986
; Patent No. 6359198
; Patent No. 6359198
; GENERAL INFORMATION:
; GENERAL Strabala, Timothy
; APPLICANT: Nieuwenhuizer, Niels
; TITLE OF INVENTION: compositions Isolated from Plant Cells
; TITLE OF INVENTION: compositions is not the Modification of Plant Cell Signalling
; FILE REPERENCE: 11000/1020
; CURRENT FILING DATE: 1999-01-12
; UNDMER OF SEQ ID NOS: 130
; SOFTWARE: PastSEQ for Windows Version 3.0
; SOFTWARE: PastSEQ for Windows Version 3.0
; SOFTWARE: ADMINISTRATION CONTINUED TO A TOWN TO 7.0
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                                                          GAGCAGATGTTGGTCTATGAATATATGCCTAACGGGACGCTCAGGGATAGCTTGACAGGA
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                                       1027 AAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGGCTTCACCTCCATGGC
                                                                                                             GAGGGACGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCTGCTAAA
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Pred. No. 5.7e-34;
0; Mismatches 274;
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Best Local Similarity
Matches 368; Conserv
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TYPE: DNA
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APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwerhuizen, Niels

TITLE OF INVENTION: Compositions Isclated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling

FILE REFERENCE: 11000/1020

CURRENT APPLICATION NUMBER: US/09/228,986

CURRENT FILING DATE: 1999-01-12

NUMBER OF SEQ ID NOS: 130

SOFTWARE: FastSEQ for Windows Version 3.0
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   1476 TCTGCAAGAGGTCTCCTCCTTGCATGA_CATGTGATCCTAAGATTATTCACCGGGAT 1535
                                       ATCAAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGT 1257
                                                                                                                                                  1596 TIGGCAAAACIIAIGGAIIAIAAGGACACACAIGIIACGACGGCIGIICGIGGAACCAII 1655
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                                                              CITGCTAAGATIGCTTCIGATACAACACGCATGTATCAACACGTGTGATGGGAACCTTT
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Pred. No. 7.4e-35;
0; Mismatches 281;
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ilarity 55.3%;
Conservative (
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US-05-228-986-9
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Best Local Similarity
Matches 360; Conserv
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US-09-228-986-9
                                       1198
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                                                                                                                                                                                                AUTHORS: GCRING, DAPHNE
AUTHORS: RCTHSTEIN, STEVEN J.
TITLE: THE S-LOCUS RECEPTOR KINASE GENE IN A
TITLE: SELF-INCOMPATIBLE BRASSICA NAPUS LINE ENCODES
TITLE: FUNCUTIONAL SERINE/THREOWINE KINASE
RELEVANT RESIDUES IN SEQ ID NO: 1: FROM 1 TO 2749
                                                                                                                                                                                                                                                                                                                                                                                                    266;
                                                                                                                                                                                                                                                                                                                                                          8.6%; Score 166.4; DB 1.
Larity 56.4%; Pred. No. 6.6e-32;
Conservative 0; Mismatches 266
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; Patent No. 6245969
                                                                                                  S-locus
                    Brassica napus
                                                            Z
                                                                                                                                                PUBLICATION: I.,2574
PUBLICATION INFORMATION:
AUTHORS: GCRTMC
                                   STRAIN: oleifera
INDIVIDUAL ISOLATE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; GENERAL INFORMATION:
; APPLICANT: Chong, Joane
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Matches 352; Conserv
  ORIGINAL SOURCE:
                    ORGANISM:
STRAIN: O
                                                                                                                     FEATURE:
NAME/KEY:
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US-08-881-706-1
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                                       1078 CTCCATGGCGAGGGACGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGA 1137
                                                                           1370 GATCATATTAATGGAAAGCTTGCCCTGGACTGGCCTACTCGCAAGCGTATAGCCCTTGGA 1429
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                                                                                                                       1138 TCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGAT
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PSPLICANT: Goring, Daphne
TILLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIBLE BRASSICA NAPUS LINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,628
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0 W. Madison St. Suite 3400
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/959,945
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/847,564 FILING DATE: 03-MAR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Pochopien Ph.D., Donald J. REGISTRATION NUMBER: 32,167
TELECOMMUICATION INFORMATICN:
TELEPHONE: 312-707-8889
TELEPRAX: 312-707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/08265628
Patent No. 5821094
GENERAL INFORMATION:
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CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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OPERATING SYSTEM:
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HYPOTHETICAL: D
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US-08-265-628-1
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                8.4%; Score 162.4; DB 4; Length 4104; 55.4%; Pred. No. 7.9e-31;
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                                                                                                                                                                                                                                                                                0; Mismatches 296;
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APPLICANT: Li, Jianming TILLS OF INVESTION: RECEPTOR KINASE BINIFILE REFERENCE: 07251/022001 CURRENT APPLICATION NUMBER: US/08/881,706 UNRENT FILING APTE: 1957-06-24 NUMBER OF SEQ ID NOS: 2 SOFIWARE: PATENTLY VEY: 2.0
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                     ORGANISM: Arabidopsis sp
                                                                                                                                                                                                     (97)--(3687)
                                                                                                                                                                                                                                                               Best Local Similarity
Matches 382; Conserv
                                                                                                                                                                                     NAME/KEY: CDS
                                                                                                                        LENGTH: 4104
                                                                                                                                                                                                   ; LOCATION: (
US-08-881-706-1
                                                                                                                                                                                                                                                                                                                                                                                                                                    806
                                                                                                                                        TYPE: DNA
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                                                                                                         SEQ ID NO 1
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Sequence 9, Application US/07717331F Patent No. 5484905

US-07-717-331F-9

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ACAGGCATCTGGTGTTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTTGTCT 1042
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             803 INGCINGAGCCACCAATGGITICICGGAGCGAACTTGTTAGGACAAGGCGGGTTCGGTT
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                                                           A Receptor Protein Kinase Gene
Rncoded At The Self-Incompatability Locus
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APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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4.6%; Pred. No. 5.4e-27;
ve 0; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/07/717,331F
                                                                                                                                                              ADDRESSEE: Yahwak & Associates
STREET: 25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/77
FILING DATE: June 19th 1991
                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.6%;
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LENGTH: 2571 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
                                                                                                             NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                             STATE: Connecticut
                                                         TITLE OF INVENTION:
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                                                                                                                                                                                      STREET: 25 SKy CITY: Trumbull
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                                                                                                                                                                                                                                                                                              06613
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1220 IAGATTICAAGITIGAAGCIAAGGIIGCIGAITTIGGTCIIGCIAAGA---TIGCIICIG 1276
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                             1043 ATGASTTTGTTCCTAACAACAATCTCGAGCTTCACCTCCATGGCGA---GGGACGGCCTA 1099
                                                                                                                                                                                                                   TTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATCAAGGCTTCAAACATATTGA 1219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2102 ACGCAATGTATGGGATATTCTCGGAAAAATCAGATGTTTTCAGTTTTGGAGTCATAGTTC 2161
                                                                         1802 ATGAGTATTTGGAAAATTTAAGCCTTGATTCTTATCTCTTTGGTAAAACCCGAAGGTCTA 1861
                                                                                                                                                                    1862 AGCTAAATTGGAATGAGAGATTCGACATTACCAAFGGTGTTGCTCGAGGGCTTTTATATC 1921
                                                                                                                                                                                                                                                               1922 ITCATCAGAGACTCACGGITTAGGATAATCCACAGAGAITFGAAAGTAAGTAACAITTTGC
                                                                                                                                                                                                                                                                                                                                         ATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGGTACTTGGCTCCGGAAT
                                                                                                                           CAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCTTATC
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APPLICANT: Wang, Guo-Liang
APPLICANT: Song, Wen-Yuang
APPLICANT: Song, Wen-Yuang
APPLICANT: Szabo, Veronique
TITLE OF INVENTION: Procedures and Materials for Conferring
TITLE OF INVENTION: Disease Resistance in Plants
NUMBER OF SEQUENCES: 27
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO COMPATIBLE
OPPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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ADDRESSEE: Townsend and Townsend and Crew Lill
STREET: Two Embarcadero Center, Eighth Floor
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17-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PUCCE APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
FILING DATE: 17-JAN-1995
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/567
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: BASTIAN, KEVIN L.,
REJISTRATION NUMBER: 34,774
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California
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                                                                                        ATACAAACACGCATGTATCAACACGTGTGAIGGGAACCTTTGGGTACTTGGCTCCGGGAT 1336
                                  2042 ACGARACGGAAGCTAACACAATGAAGGTGGTCGGAACATACGGCTACATGTCCCCGGAAT 2101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 2833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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Pred. No. 5.6e-27;
0; Mismatches 274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/07/717, 331F
FILING DATE: June 19th 1951
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/0717331F Patent No. 5484905
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Yahwak & Associates
STREBT: 25 Skytop Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: George M. Yahwak
REGISTARION NYBABE: 26,824
TELECHMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   1397 TGGAGCTCATTACTGGA 1413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM IYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word
CURRENT APPLICATION DATA:
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NAME: George M. Yahwak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 2833 base pairs
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Best Local Similarity 54.6'
Matches 337; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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MEDIUM IYPE: Floppy I
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STATE: Connecticut
COUNTRY: USA
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; MOLECULE TYPE:
US-07-717-331F-1
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US-07-717-331F-1
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CORRESPONDENCE ADDRESS: ADDRESSE: Tahwak & Associates
STRRET: 25 Skytop Drive CITY: Trumbull
                                                                                                                                                                                                            Length 1554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua APPLICANT: Stein
                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                       Score 140.6; DB 2;
Pred. No. 1.3e-25;
0; Mismatches 274;
REFERENCE/DCCKET NUMBER: 023070-058940US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/07717331F Patent No. 5484905
GENERAL INFORMATION:
          TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 576-0200
TELEFAX: (415) 576-0300
INPORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 1554 Dase pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: cDNA (partial)
                                                                                                                                                                                                          7.28;
                                                                                                                                                                                                     Query Match
Best Local Similarity 53.44
Matches 318; Conservative
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US-08-587-680A-24
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53.8%; Pred. No. 2.7e-25;
tive 0; Mismatches 282;
                                                                                                                                                      APPLICATION NUMBER: US/07/717,331F
FILING DATE: June 19th 1991
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: GEOTGE M. YAHWAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2173 TTGCTTCTTGAAATTATAAGTGG 2195
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                                                                                                                                                                                                                                                     NAME: George M. Yahwak
REGISTRATION NUMBER: 26,824
                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
TELEFAX: (203)268-1951
                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: Macintosh
OPERATING SYSTEM: MS-DOS
SOTTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2749 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Matches 335; Conservative
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US-07-717-331F-4
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Sequence 10, Application US/09228986 Patent No. 6359198 GENERAL INFORMATION:
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; ORGANISM: Pinus radiata
US-09-228-986-10
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                           LENGTH: 2336
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                                     GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Mieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
CURRENT APPLICATION VUBBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
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                                                                                                                                                                                                                                                                                                         0; Mismatches 383; Indels
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                                                                                                                                                                                                                                                                                            Pred. No. 6.4e-25;
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               Sequence 1, Application US/09228986
Patent No. 6359198
                                                                                                                                                                                                                                                                                          Best Local Similarity 50.9
Matches 425; Conservative
                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Pinus radiata
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APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
FILE REFERENCE: FASTEQ FOR Windows Version 3.0
                                                       1953
1539 TESGTATGACAGAGAGAGATGGCTCSCATGGTTGCTTGTGCTGCGGCTTGTGTTCGCCA 1598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    787 ITCACATACGAGGAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTGGTAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         847 CAAGGCGGGTTCGGTTACGTGCACAAGGTGTGTTGCCTAGT---GGGAAAGAAGTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1024 GCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGGAGCTTCACCTCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1144 AAAGGACTITCTTATCTTCATGAAGATTGCAAICCTAAAATCATICACCGTGATATCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1204 GCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTTGGTCTTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1264 AAGATIGCITCIGATACAAACACGCATGTATCAACACGTGTGATGGGAACCITTGGGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1504 CGCCTGTATGATCACAGTGAGAATCCGGAGACGACATATGTGTAGGAACGTTGGGGGTAC
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                                                                                                                                  1954 ATCTCCTCAGCAACGCCCTAAAATGAGCCATGTGTGTGAGGGTGATTCAAGACATT
                                                                                                      TECAGCTCGCCGCAGACCTCGCATGAGCCAGATTGTGCGCTGCGTTAGAAGGAAAT
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Pred. No. 4.4e-23;
0; Mismatches 337;
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us-10-086-464-1.rni

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APPLICANT: Tanksley, Steven D.

PEDLICANT: Marth, Gregory B.

APPLICAN MARTHON: GENE CONFERRING DISEASE RESISTANCE

TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRULENCE GENE IN PLANT PAIN
1050 TGTTCCTAACAACTACTCGAGCTTCACCTCCATGGCGAGGGACGGCCTACAATGGAATG 1109
                                                                                1110 GAGCACCAGAITGAAGAITGCICITGGATCTGCIAAAGGACITTCITAICITCAIGAAGA 1169
                                                                                                                                                                                                                                                            1286
                                                                                                                                                                                                                                                                                                                                        1287 GCAIGTAICAACACGIGIGAIGGGAACCITIGGGIACIIGGCICCGGAAIACGCIGCAAG 1346
                                                                                                                                                                                                                                                                                                                                                                                                                             1347 CGGAAAGCICACGGAGAAGICIGACGITTICICATTIGGCGTIGIGCTTITGGAGCICAI 1406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1407 TACTGGACGTCGACCCGTTGATGCCAACAATGTCTATGTAGATGACAGCTTAGTTGACTG 1466
                                                                                                                                                                                                                                                                                                                                                                                  585 CCAICTTAGCACAGTAGTGAAAGGAACTCTCGGCTACATTGACCCTGAATATTTTAAAA 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                          645 GGGACGACTCACTGAAAATCTGATGTTTATTCTTTCGGTGTTGTTTTATTCGAGTTCT 704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          705 TIGIGCIAGGICIGCCAIAGIICAAICTIICCAAGGGAGAIGGIIAATIITAGCIGAAIG 764
                                          348 CAIGGAGAATGGGAACCICAAGAGACAITIGIAIGGAICAGAICIACCCACAAIGAGCAI
                                                                                                                 1170 IIGCAATCCIAAAATCATTCACGIGATATCAAGGCTICAAACATATIGATAGAITTCAA
                                                                                                                                                                                             1230 STITGAAGCTAAGGIIGCTGAITITGGICTTGCTAAGAITGCTICTGA---TACAAACAC
                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/111,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,185
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08447185 Patent No. 5648599
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TELECOMUNICATION INFORMATION:
TELEFRONE: (716)-263-1000
TELEFRA: (716)-263-1600
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             765 GGCAGTGGAGTCGCATAA 782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: ATTORNEY/AGENT INFORMATION:
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STRANDEDNESS: double
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CORRESPONDENCE ADDRESS:
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CITY: Rochester
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COUNTRY: U.S.A.
2IP: 14603
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TO AN AVIRULENCE GENE IN PLANT PATHOGE
             1384 GGCGTTGTGCCTTTTGGAGCTCATTACTGGACGTCGACCGTTGATGCCCAACAATGTCTAT 1443
                                        990 ICTGGTGTCTCTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTTGTCTATGAGTT 1049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                810 AGCCACCAATGGTTTCTCCGAGGCGAACTTGTTAGGACAAGGCGGGTTCGGTTACGTGCA 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           108 AGCAACTAATAATTTTGATCACAAGTTTTTAATTGGACATGGTGTCTTTGGGAAGGTTTA 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     870 CAAAGGIGIGIIGCCIAGIGGAAAGAAGIIGCIGIGAAGCAGIIGAAAGIIGGGAGIGG 929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          930 TCAGGGAGAGAGGGAGTTTCAGGCAGAGGTTGAGATCATCAGCAGAGTTCACCACAGGCA 989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 ACAAGGTAITGAAGAGTTCGAAACAGAAATTGAGACTCTCTCATTTTGCAGACATCCGCA 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168 CAAGGGTGTTTTGCGTGATGGAGCAAAGGTGGCCCTGAAAAGGCGTACACCTGAGTCCTC 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       288 TCTGGTTTCATTGATAGGATTCTGTGAAAGAAATGAGATGATCTAATTTATAAATA 347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6.2%; Score 121.2; DB 1;
50.7%; Pred. No. 7.1e-21;
tive 0; Mismatches 328;
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Tanksley, Steven D.
APPLICANT: Martin, Gregory B.
TITLE OF INVENTION: GENE COMFERRING DISEASE
TITLE OF INVENTION: TO PLANIS BY RESPONDING
                                                                                                                          1684 GAGCGCAIGATTTTAGTGGAGTGGGC 1709
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 80C
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/111,078
                                                                                                1444 GTAGATGACAGCTTAGTTGACTGGGC
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APPLICATION NUMBER: US/08/447,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Goldman Mr., Michael L.
TELECOMUNICATION INFORMATION:
TELEPHONE: (716)263-1000
TELEFAX: (716)-263-1600
INFORMATION FOR ESQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 966 base pairs
                                                                                                                                                                                                                                               Sequence 2, Application US/08447185
Patent No. 5648599
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 50.79
Matches 344; Conservative
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: Climing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCAT 1492
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                                                                                                                                      901
                                                                                                                                                                                                                                                                                   962 AGAICAICAGCAGAGTICACCACAGGCAICTGGGGTGTCTTGTTGGTTATTGCATCGCCG
                                                                                                                                                                                                                                                                                                                                                            1022 GIGCCAAAAGAIIGCIIGICIAIGAGIIIIGIICCIAACAACAAICICGAGCIICACCICC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 842 TAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGGTTGCCTAGTGGGAAAGAAGTTG
                                                                                                                                                                                                            2062 CIGIGAAAGIGCGGTIIGAIAAAACCCAACIIGGIGCAGAIICTIICAIAAAIGAGGIIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1136 GATCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAAATCATTCACCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2362 ACATCAAGTGCAGTAATATATAGGACAAGGAGATGAATGCAAGACTTTGCGACTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTCTTGCTAAGATTGCTTCTGATACAAAC---ACGCATGTATCAACACGTGTGATGGGAA
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                                                             Length 3097;
                                                                                                    Indels
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APPLICANT: Oshima, Junko
APPLICANT: Mulligan, John T.
APPLICANT: Schellenberg, Gerald D.
TITLE OF INVENTION: GENE AND GENE PRODUCTS RELATED TITLE OF INVENTION: WERNER'S SYNDROME
UNDMER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
                                                           Score 117.8; DB 4;
Pred. No. 8.5e-20;
0; Mismatches 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
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                                                           Query Match 6.1%;
Best Local Similarity 50.4%;
Matches 346; Conservative
       ; ORGANISM: Eucalyptus grandîs
US-09-228-986-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Fu, Ying-Hui
APPLICANT: Yu, Chang-En
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STREET: 63/
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APPLICANT: Strabbla, Timothy
APPLICANT: Strabbla, Timothy
APPLICANT: Nieuwenhuizen, Niels
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 11
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                                                           Length 2443;
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                                                           DB 1;
                                                     Score 121.2; DB 1;
Pred. No. 1.1e-20;
); Mismatches 328;
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Patent No. 6359198
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 DNA (genomic)
                                                   6.2%;
ilarity 50.7%;
Conservative (
                                                                       Similarity
; MOLECULE TYPE:
US-08-447-185-3
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LENGTH: 3097
TYPE: DNA
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Best Local
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184 TCTCCACCAACTCCATCTACGCCGGGATCTCCACCTCCTCTTCCTCAGCCGTCTCCACCC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 6.1%; Score 117.8; DB 3; Length 1 Best Local Similarity 63.0%; Pred. No. 1.8e-19; Matches 182; Conservative 0; Mismatches 107; Indels
                        ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 27-DEC-1996
CLASSIFICATION: 8000
                                                                                                                                                                               ATTORNEY AGENT INPORATION:
NAME: No. 6090520tenburg Ph.D., Carol REGISTRATION NUMBER: 39,317
REFERENCE/COCKET NUMBER: 39,317
REFERENCE/COCKET NUMBER: 240052.419
TELEPHONE: (206) 62-4900
TELEPHONE: (206) 62-4900
TELEPHONE: (206) 62-6031
INFORMATION FOR SEQ ID NO. 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 16442 base pairs
TYPE: nucleic acid
STRANDENDENS: Single
 Washington
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STATE: W
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Search completed: July 7, 2003, 07:26:59 Job time : 119 secs

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GenCore version 5.1.6
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AXO88875 Sequence AYO2899 Brassica AYO2899 Brassica AYO2899 Brassica AYO5788 Arabidops AYO5705 Arabidops AYO5901 Arabidops AYO89024 Arabidops AXO88882 Sequence AXO88882 Sequence AXO88885 Sequence AXO88885 Sequence AXO88888 Sequence AXO88888 Sequence AXO88888 Sequence AXO88888 Sequence AXO88888 Sequence AXO88888 Sequence AXO88889 Sequence AXO88889 Sequence AXO88899 Sequence AXO8697 Arabidops AYO5625 Arabidops AYO66344 Oryza sat AXO88879 Sequence AXO88879 Sequence AXO869344 Oryza sat AXO869344 Oryza sat AXO88879 Sequence AXO83963 Arabidops AYO63963 Arabidops AYO63963 Arabidops AYO63963 Arabidops AYO63963 Arabidops AYO63963 Arabidops AYO63963 Arabidops AYO63964 Arabidops AXO93964 Arabidops AXO93964 Arabidops	AF367265 Arabidops AY04968 Arabidops AZ27703 zea mays AX461250 Sequence AC02330 Arabidops AL161494 Arabidops AY087491 Arabidops AY125315 Arabidops AX125315 Arabidops AX125315 Arabidops	NA linear PAT 17-MAR-2001 rta; Embryophyta; Tracheophyta; tryledons; core eudicots; brassicaceae; Brassica.
SUMMARIES OGTH DB ID	·	αααααααααα	1944 bp 1 W00114563. 9 ae; Streptophyphyta; eudicchrasicales; Elike receptor
% Query core Match	1944 1944 1969 1944 100.0 1969 100.0	2011 100.1 100.0 100.0 100.0 100.0 100.0	AX088876 Sequence 1 from Patent AX088876 AX088876.1 GI:1339763 rape. Brassica napus Eukaryota; Viridiplant, Spermatophyta; Mapnoli, Rosidae; eurosids II; ) 1 (bases 1 to 1944) Goring, D. and Silva, N. Proline-rich extensin-
Result No. S			RESULT 1 AXOB8876 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

661 CCACGGCAACCTCCACCTCCACCCCCTTTCATGACCAGCGGCGGCTCCGAC 720 [] [] [] [] [] [] [] [] [] [] [] [] [] [	961 GAGATCARCAGCAGGTTCACCAGGCATCTGGTGTTTTTTTTTT	1081 CAIGGCAGGGACGCCTACAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140 1111111111111111111111111111111111	AAGGCITCAAACATATIGAIAGAITTCAAGTITGAAGCIAAGGTIGCIGAITTIGGICTI 126 	GCTAAGATIGCTTCTGAIACAAACACGCAIGIAICAACACGIGIGAIGGGAACCTTTGGG 132	AAGTCE AAGTCE AAGTCE STEGAE	1381 ITTGGCGTTGTGTTTGGAGCTCATTACTGGACGTCGACCGTTGATGCCAACAATGTC 1440 1441 TATGTAGATGACAGTTAGTTGACTGGCCACGACCATTGCTTAACCGAGCATTGACTTGACTTGACAA 1500 1441 TATGTAGATGACAGTTGACTGGCCACGACCATTGCTTAACCGAGCATTGAA 1500 1441 TATGTAGATGACAGTTAGTTGACTGGGCCACGACCATTGCTTAACCGAGCATCTGAGCAA 1500	1501 GGAGACTTTGAGGGTTTAGCTGATGCAAGATGAATAATGGGTAIGACAGAGAGAGTG 1560 	1561 GCTCGCATGCTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGC 1620 	1621 ATGASCCAGAITGTGGGGGGTTAGAAGGAAAIGTATCACTGTCAGATCTTAACGAAGGG 1680 [	1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTCG 1740 11   1   1   1   1   1   1   1   1   1
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JOURNAL Patent: WO 0114563-A 1 01-MAR-2001;  Goring, Daphne (CA); Silva, Mancy (CA)  Location/Qualifiers  1 . 1944  /Organism="Brassica napus"  /D_xref="taxon:3708"  1 . 1944  /Orden="unnamed protein product" /codo_start=1 /protein_in="cataron" /protein="cataron" /protein="cat	BASE COUNT 464 a 550 c 459 g 471 t ORIGIN  QUERY Match  Query Match  Best Local Similarity 100.0%; Pred. No. 0;  Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	1 ATGTCCTCGGCGCCGTCTCCGGGGACTGGTTCGCCTCCATCTCCACCATCAAACTCCAA 60	29 121 CCATCCACTATTCCGACATCTCCTCCTCCTCCTCCTCCTCTTCTCCTCCCCCCC 120 29 121 CCATCCACTATTCCGACATCTCCTCCTCTTCTCGCTCTACACCTTCTCCTCCT 180  121 CCATCCACTATTCCGACATCTCCTCCTTCTTCTCGCTCTACACCTTCTTCTTTTTTTT	OY 181 CCATCTCCACAACTCCATCTACGCGGGATCTCCACTTCCTCTCAGCGTCTCCA 240	QY 241 CCGGTCCAACTAGGCGGGATCTCCACTGTTACTCCTCCTACTCGAAACCCT 300	301 CCACCTTCAGTCCCAGGACCACCTCCAATCCTTCACGGAAGGAGATCTCCTCGACCT 36 361 CCACCTTCTCCCTCGCCGCCGTCCATCTTCCGACGGTTTATCAACAGGATGGTGGTG 42 161	CICTGT 48	OY 481 AAGAAGAAAGGAGGAGGAAGAAGATGCTTACTATGCTCCGCCACCTCCTCT 540	OY 541 GGTCCCAAAGCCGAGGACCTTACGGTGGACAGCAACAACAATGGCGGCAACAAAAGCGC 600	OY 601 ACACCACCGTCAGATCATGTCGAGCGTCACCACCACCGAGGCTCCATCTCCA 660 [11111111111111111111111111111111111

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ACCACCACTCCTCCAGCTTCCGCTCCTCCCACCACCACCACCACCACCACCACCACCACCAC	301 CCACCTTCAGGACCACGACTCCAAGGAGGATCTCCTCCACCT 360 310 CCACCTTCAGGCAAGGAGCACCTCTCAGGCAAGGAGGATCTCCTCCACCT 360 397 CCACCTTCAGGCACCACGACCACCTCCATCAGGCAAGGAGGATCTCCTCACCACCT 456 361 CCATCTTCAGGCACCACCTCCTCTCTCCCACGCACTATCAACAGGAGTGGTG 420 111111111111111111111111111111111111	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 NOTATION OF THE STATE OF THE	1021 GGTGCCAAAAGATTGCTGTGTGTGTTGTTCCTAACAACATCTCGAGCTTCACCTC 1080
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1741   AGCCAGTACAATGAAGACATGAAGAAGTTAAGGAAAATGGCACTTGGAACTCAAGAGTAC   1800   1741   AGCCAGTACAATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTAC   1801   1741   AGCCAGTACAATGAAGAACATGAAGAATAGGAAAATGGCACATTGGAACTCAAGAGTAC   1801   AACGCCACGGGTGACATACAGACAACTAATGCAACTTACACATTACAACTTACACATTACAACTTACACATTACAACTTACACACTTACACACTTACACACTTACATTACAACA	AY028699 AY028699 AY028699 LOCUG DEFINITION Brassica napus receptor protein kinase PERKI mRNA, complete cds. ACCESSION AY028699. GI:13447448 KEYWORDS SOURCE ORGANISM Brassica napus CRGANISM Brassica napus EMEFERENCE ORGANISM REFERENCE 1 (bases 1 to 2189) Brassicales; Brassicae; AYDERGION AY028699. GI:13447448  KEFERENCE 1 (bases 1 to 2189)	AUTHORS Silva, N.F. and Goring, D.R.  IITLE Characterization of a novel Brassica napus receptor protein kinase  JOURNAL Upublished  REFERENCE 2 (bases) 1 to 2189)  AUTHORS 511va, N.F. and Goring, D.R.  TITLE Direct Submission  JOURNAL Submitted (19-MAR-2001) Biology, York University, 4700 Keele  FEATURES  Location/Qualifiers  Street, Toronto, Ontario M3J 1P3, Canada  L. 2189  CDS //Organism="Brassica napus"  //db xref="taxon:3768"  //db xref="taxon:3768"  //db xref="teceptor protein kinase PERKI"  //protein_id="AAK21965.1"	/db_xref="G1:13447449"  /db_xref="G1:13447449"  /db_xref="G1:13447449"  /db_xref="G1:13447449"  /db_xref="G1:1347449"  /db_xref="G1:13474449"  /db_xref="G1:1347449"  /db_xref="G1:13474449"  /db_xref="G1:13474449"  /db_xref="G1:10="Massapered specific property proproperty property p	Query Match  Dest Local Similarity 100.0%; Pred. No. 0;  Matches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Atches 1944; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  QY 1 ATGTCCTCGGCGCTCTCCGGGGATGGTTCGCCTCCATCTCCATCAAACTCCACA 60

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Shinozaki,K., Ecker,J., Theologis,A. and Davis,R.W.
Direct Submission
Submitted (01-JUL-2002) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94361,
                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members constructed as sequenced the pUNI (ORF) clones using the RAFL cDNAs: Tripp,M., NGUYEN, Southwick,B., Karlin-Neumann,G., Lam,B., Miranda,M., Palm,C.J., Bowser,L., Jones,T., Banh,J., Chen,H., Cheuk,R., Chung,M.K., Kim,C., Lin,J., Liu,S.X., Phan,P.K., Sakano,H., Shinn,P., Yamada,K., Ecker,J., Theologis,A. and Davis,R.W.
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1. 2098
/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
                                                                                                                                                                          collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKI Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                e-mail for correspondence: arab@sequence.stanford.edu
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llarity 83.4%; Pred. No. 1.7e-265;
Conservative 0; Mismatches 291;
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SET_COND.

Arabidopsis thaliana

Enkaryotya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core endicots;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

CE (bases 1 to 2098)

Tripp, M., Southwick, A., Karlin-Neumann, G., Nguyen, M., Miranda, M., Palm, C.J., Bowser, L., Jones, T., Banh, J., Carningl, P., Chen, H., Cheuk, R., Chung, M.K., Rayashizakl, Y., Ishida, J., Kamlya, A., Kawai, J., Kim, C., Lin, J., Liu, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K.,
                                         TACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCA 1380
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Arabidopsis thaliana protein kinase-like protein mRNA, complete
           AAGGCTTCAAACATATTGATATTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT
                                                                                                                  GCTAAGATTGCTTCTGATACAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGG
                                                                                                                                                                                                                                                                                                                                                           GCTCGCATGGTTGCTTGTGCTGCGCTTGTTCGCCATTCAGCTCGCCGCAGACCTCGC
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Db 1348 GAATAIGCIGCAAGTGGAAAGCICACAG  Qy 1393 CTITGGAACICATTACTGGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCG	QY 1573 GCTTEIGCTGCGCTTGTGTTCGCCCATT	OY 1693 CAAAGCAATGTATACAGCTCATACGAG	1828 1873 1898 1933	RESULT 4 AY055788 LOCUS AY055788 AY055788 AY055788 AXABIGOPSIS thaliana AI3924550, ACCESSION AY056788 I GI:15983764 AYABIGOPSIS thaliana SOURCE ARABIGOPSIS thaliana ORGANISM EUkaryota; Viridiplanatae; Streg	Residae; eurosids II; Brassica, Cheuk, R., Chen, H., Kim, C.J., Ke BOWSER, L., Carnindi, P., Dale, S. Ishida, J., Lan, B., Lee, J. M., Lin Narusaka, M., Nguyen, M., Oncders Ouach, H.L., Sakurai, T., Satou, M. TOTIUM, M., Yamada, K., Yamanura Davis, R.W., Theologis, A. and Ec Arabidopsis cona. Clones JOURNAL Upublished REFERENCE (Chauk, R., Chen, H., Kim, C.J., Kc BOWSER, L., Carninci, P., Dale, J. Ishida, J., Jiang, P. K., Jones, T., Kawai, J., Lam, B., Lee, J. M., Lin Narusaka, M., Nguyen, M., Oncdera Ouach, H.L., Sakurai, T., Satoi, M.
268 CCACCGTCTCCACCCACACCTCAAACCTCGAAGCCTCCATCTCTAACCAAGGACA 327 322 CCGTCCAATCCTTCACGCGAAGGAGGTCTCCTCGACCTCCTCGCCCCG 381 1			CAGITTCITCUCACGETCAGGGGTTGTGTTAGGCTTCCCAAAGCACTTTCACA CGGTTCTTCCTCCACCATCTCAGGGGTTGTTAGGCTTTTCCAAAGCACTTTCACA CCGGTTCTTCCTCCACCATCTCCAGGGGTTGTTAGGGTTTTTAAAGCACTTTCACT TACGAGGAGTAGTTGTCAGGGCTTTCTCCAGGGGAACTTTTAGGACAAGGGTTTCACT TATGAGGAGTTGTCAGAGCCACCAATGGTTTTTTTTTT	TTGAAGTTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1093 GGGCCTACAATGGAATGGAGTTGAAGATTGCACTTGGATCTGCTAAAGGACTT 1152 1108 CGGCCTACAATGGAATGGAGTTGAAGATTGCTCTTGGATCTGCTAAAGGACTT 1157 1108 CGGCCTACGAATGGAATGGAATTGAAGTTGCTCTTGGATCTGCTAAAGGACTT 1167 1153 TCTTATCTTCATGAAGTTGCAATCCTAAAATCATTCACCGTGATATCAAGGCTCAAAC 1212 1168 TCATATCTTCATGAAGATTGCAATCCTAAAATCATTCACGTGATATTAAGGCGTCAAAC 1227 1213 ATATGATAGATTCAAGTTTGAAGCTAAGGTTGCTGATTTGGTCTTGCTAAACTTGTT 1227 1228 ATATGATACAAATTTGAAGCTAAGGTTGCTGATTTGGTCTTGGCTCGG 1332 1238 TCTGATACAAAACACGCATGTAACAACTGGGTGATGGGTCCG 1347 1238 TCTGATACAAAACACCTATGAACTAACAACTGAGGTACTTGGCTCCG 1347 1238 GAATACGCTGCAAAACTAACAACTAACAACAACAAGAATCAACAACAACAACAACAACAACAACAAAAAAAA
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e.J.M., Goldsmith, A.D., Hayashizaki, Y.,
ss.T., Kamiya, A., Karlin-Weumann, G.,
Lin, J., Liu, S.X., Miranda, M.,
dera, C.S., Palm, C.J., Pham, P.K.,
ou, M., Seki, M., Southwick, A., Tang, C.C.,
d Ecker, J.R. FGGGTATGACAGAGAGGAGGTGGCTCGCATGGTT 1572 1632 1692 AGAAAAGTCTGACGTTTTCTCATTTGGCGTTGTA 1407 GCACTTGGAACTCAAGAGTACAACGCCACGGGT 1812 AAGATTAAGAAAACCGGICAAGGTTATAGTGGA 1947 AAGATTAAGAGAACCGGTCAGGGTTATAGTGGA 1932 bp mRNA linear PLN 08-OCT-2001 0/MOB24\_8 mRNA, complete cds. Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jiang, P.X., Jones, T., Kamiya, A., Karlin-Neumann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Pallm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satoi, M., Seki, M., Southwick, A., Tang, C.C., eptophyta; Embryophyta; Tracheophyta; eudicotyledons; core eudicots; ales; Brassicaceae; Arabidopsis. SCTTAACCGAGCATCTGAGCAAGGAGACTTTGAG TTCAGCTCGCCGCAGACCTCGCATGAGCCAGATT ACTGTCAGATCTTAACGAAGSGATGAGACCAGGT

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Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.
Divis, E.W., Theologis, A. and Ecker, J.R.
Direct Submitssion
Submitted (11-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                            Collection and clustering of RAFL CDNAs (RAFL CDNA : 'RIKEN Arabidopsis Full-Length CDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPGHSNVYSSYGGSTDYDTSQYNDDMIKFRKMALGTQEYGTTGEYSNPTSDYGLYPSG
                                                                                                                                                                                                                                                      The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Taian, P.X., Jones, T., Karlin. Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Onodera, C.S., Palm, C.J., Pham, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally this work. Shinozaki, R. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIS.

Location/Qualifiers
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C; Mismatches 291;
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                                                                                                The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Bowser, L., Jand, P., Banh, J., Chen, H., Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S. X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                     Nguyen,M, (SSP/Stanford) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Davis,R.W. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers
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Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA,
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Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M., Palln, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Kawai, J., Kim, C., Lio, J., Lit, S.Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lio, J., Lit, S.X., Narusaka, M., Pham, P.K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Ecker, J., Theologis, A. and Davis, R.W.
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Submitted (22-OCT-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
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1. 2190
/organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromcsome=13" /chromcsome=13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90
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     and Davis, R.W.
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Pred. No. 1.7e-265;
0; Mismatches 291;
   Theologis, A.
                                                                                                                                                                                                                      /gene="At3g24550"
30. 1988
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/gene="At3g24550"
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Best Local Similarity 83.4%;
Matches 1611; Conservative (
 Ecker, J.,
Yamada, K.,
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PSPSTMSTSPPPSSPLPPSPPSPPSPPSPPSPPTPSPPPTTPSSPP
PSPNGCPPNTPSGSTPRTPSPPSPPSPSPGSLGTGVWOTALIGGTALLULICL
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HIVSLIGTANGVQULLYFEVPNNEEFHLHGKGRPTMEWSTRLKIALGSAKGLSTL
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YAASGKLITEKSDVFSFGVYLLELITGRRPVDANNYYDDSLYDWARPLINRASFEGDF
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RPGHSNVYSSYGGSIDYDTSQYNDDMIKFRKMALGTQEYGTTGEYSNPTSDYGEYPSG
SSSEGQATREMEMSKIKKTGQGYSGPSL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            146 TCTCCACGETCTCCTCCCACAAGTCGACCACCACCACCTCCTCCAGCAGCCTCTTCT
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Pred. No. 3.7e-265;
0; Mismatches 292; Indels
                                                                                                                                                                                                                                                                                                                          /product="protein kinase-like protein"
/protein_id="AAK43886.1"
/db_xref="GI:13877617"
                                                                                   /note="This clone is in pBluescript
ecotype: Columbia"
1, .2557
/gene="MoB24.13"
107. .2065
                                                           /clone="RAFL11-07-N23"
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Matches 1610; Conserv
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SCITGCGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCAGACCTCGCATGAGCCAGALA 1676
                                                                  GAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCCACGGGT 1812
                                                                                                                                                                                                                                                                                                                                                                    GAGTACAGTAATCCGACCAGTGACTAJGGACTGTACCCGTCTGGTTCAAGCAGCGAGGGC 1872
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                                                                                                                                                                                                                                      AF370509 2257 bp mRNA linear PLN 30-APR-2001
Arabidopsis thaliana protein kinase-like protein (MOB24.13) mRNA,
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Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center,
CA 94304,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Southwick, A. (SSP/Stanford) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Davis, R.R. (SSP/Stanford) contributed equally to this work as PIS. Location/Qualifiers
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/organism="Arabidopsis thaliana"
/db_xref="taxon:3702"
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AF370509 AF370509.1 GI:13877616

FLI\_CDNA.

SOURCE ORGANISM

KEYWORDS

VERSION

REFERENCE AUTHORS Submitted

TITLE

COMMENT

complete cds.

DEFINITION

ACCESSION

RESULT 7 AF370509 LOCUS

1977 CCCTCTTTAA 1988 CCTTCTCTTTAA 1944

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Gaps

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261 373 321 433 381 493 498

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441 553 615

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Southwick, A.

scurce

FEATURES

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Matches 1998;   Conservative   0;   Kismitches 303;   Indels 23;   Gaps   5;		OY 1096 CCTACAATGGAATGGACCACATTGAAGATTGCTCTTGGATCTGCTAAGGACTTTCT 1155	QY 1156 TATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATCAAGGCTTCAAACATA 1215	OY 1216 TIGATAGATITCAAGTTAGAGTTGCTGATTTGGTCTTGCTAAGATTGCTTCT 1275	QY 1276 GATACAAACACGCAIGTAICAACAGGIGIGAIGGGAACCTITGGGTACTIGGCTCCGGAA 1335 1392 GATACAAACACTCAIGTAICTACACGCGIGAIGGGAACCTITGGGTAITTGGCTCCAGAA 1451	QY 1336 TACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTCTCATTTGGCG-TGTGCTT 1395	QY 1396 TIGGAGCICATTACTGGACGTGGACCCGTTGATGCCAACGTTGTAGATGACAGC 1455	Qy 1456 TTAGTTGACTGGGCACCATTGCTTAACCGAGCATCTGAGCAAGCA	OY 1516 TIAGCTGAIGCAAAGAIGAATAAIGGGTAIGACAGAGAGAGAGGCCCCAIGGIIGCI 1575	QY 1576 TGTGCTGCGGCTTCTGTTCGCCTTCGCCGCGGGCCCGCGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	QY 1636 CGTGCGTTAGAAGGAATGTATCACTGTCAGATCTTAACGAAGGGATGAGCCAGGTCAA 1695	QY 1696 AGCAATGTATACAGCICATACGGAGGAAGGAGCGGATTAIGACTGGAGCGGTACAATGA 1755	QY 1756 GACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCGGGGGGG 1815	OY 1816 TACAGTAATCCGACCAGTGACTATGGACTGTACCCGTCTGGTTCAAGCAGGGCCAA 1875	1876 ACCACGCGA 	OY 1936 TCTCTTTA 1944	AX088862	ION N DS	SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
	s 1598; Conservative 0; Mismatches 303; Indels 28; Gaps	31 TEGCETCCATCTSCACATCAAACTCCACACACACACTCCTCCACCTTCCGCTCTT 90 114 TOTCCACCGTCTTCACAAAAAAAAAAAAAAAAAAAAAAAA	91 CCICCCACCACCACCTTCTTCICCCCCCCACCACTATTCCACCACTTT 14	142 CCTCCTCCTTCTTCTCCTCTTCTCCTCCTCCTCCTCCATCACTABILCAACTCT 20 142 CCTCCTCCTTCTTCTTCTCTACACCTTCTGCTCCTCCATCTCCACCAACTCCATCT 20 264 CCTCCTCCTTCTTCTTCTTACACTTCTTCTTCTTCTCTCATCTTCT	202 ACGCCGGGATCTCCACCTCTCACCGTCCACCTCCACCTCCACCTCCGGGATCTTCCTCACCGTCTCCACCGTCTCCTCACCTCCACCTCCCACCTCCCGGATCTCTCCTCACCTTCTCACCTCCACCTCCCACCTCTCTCCTTCTT	262 TCTCCACCGCACTGTTACTCCTCCTACTCGAACCCTCCACCTTCAGTCCCAGGACCA	522 CCGTCCAATCCTTCACGCGAAGGAGGATCTCCTCGACCTCCATCTTCTCCCTGGCCGCCG	382 TCTCTTCTACACGGTTATACAACAGAGTGGTGGGGAATCGCCATCGGAGGAGTC 111	442 GCTCTGCTTGIGATAGTGACTCTGATTTGTCTCCTCTGTAAGAAGAACCACGGAGA 49 11	499 GACGAAGAAGTIGCTTACTTCCTCCGCCACCTCCTCGTGCTCCAAAGCCGGAGAAAAAAAA	559 CCTTACGGTGGACAGCAGCAACAACAGCAACAAAACGCAACGCGCACGGTCAT 	619 GTGGTGACGTCACTACCACCTAAGGCTCCATCTCCACCACGGCAACCTCCT	676 CCACCTCCACCACCACCACCACCACCACCACCACCACCAC	736 GTTCTTCCTCCACGTCTCCAGGGCTTGTGTTAGGCTTCTCCAAAAGCACTTCACATAC	796 GAGGAGCTAGCTAGACCCACCAATGGTTTCTCCGAGGGGAACTTGTTAGGACAAGGCGGG 85 [	856 TTCGGTTACGTGCACAAAGGTGTGTGCCTAGTGGGAAAGAGTTGCTGTGAAGCAGTTG	916 AAAGTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTTGAGATCATCAGCAGA 	976 GITCACCACAGGCALCTGGTGCTTATTGCATCGCCGGTGCCAAAGAITG 103 [	1036 CTTGFCTATGAGTTTGTTCCTAACAACAATCTCGAGGTTCACCTCCATGGCGAGGGAGG

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1690 GGICAAAGCAAIGIATACAGCICAIACGGAGGAAGCACCGATIAIGACICGAAGCAGCAGTA 1749
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Wandilophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 1939)
Goring.D. and Silva,N.
Broline-rich extensin-like receptor kinases
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                                     1417 AIGTTATTGGAACTIATAACTGGAAAACGACCGGTTGAT---AATAGCATCACCATGGAC
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                                                                                              GIGCTITIGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTCTATAGAT
                                                                                                                                                                       GACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTT
                                                                                                                                                                                                 1474 GACACCITAGTAGATIGGGCICGGCCTCTATGGCTCGCGCGCTAGAAGATGGAAACTTT
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Pred. No. 1.1e-93;
0; Mismatches 363;
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llarity 67.1%;
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OOSTGGWGGGCOPPPPRHTSGEDSSWSGPPRPPBPSALALGFRKSTFTYDE
LAAATGGTTDANLLGQGGFQYVHKGVLPPSGKEVAWSLKAGSQGEREFQAEVDIISR
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SPPSRSNCDNGGSRSSPPGDTGGSRSDNPPSSGGSSGGGGGRSNTNTAIIVGYLVGA
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Pred. No. 1.1e-93;
0; Mismatches 363; Indels 3;
             1 (bases 1 to 1902)
Goring, D. and Silva, N.
Prolline-rich extensin-like receptor kinases.
Patent: W0 0114563-A 701-MAR-2001;
Goring, Daphne (CA); Silva, Nancy (CA)
Location/Qualifiers

    1902 "Arabidopsis thaliana"
//Organism="Arabidopsis thaliana"
//Ob xref="taxon:3702"
    1902 "Arabidopsis thaliana"

                                                                                                                                                                                                          /note="upnamed protein product"
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/protein_id="CAC34705.1"
/db_xref="G1:13397646"
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TITLE
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                                                                                                                       REFERENCE
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                                                                                                                                                                                                                                                                                            COMMENT
                                                                                                                                                                                                                                                      1209
                                                                    AGCAGAGTICACCACAGGCATCTGGTGTCTCTTGTTGGTTATTGCATCGCCGGTGCCAAA 1029
                                                                                                                                                    AGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTCCATGGCGAG 1289
                                                                                                                                                                                                  1390 GGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCTGCTAAAGGA 1149
                                                                                                                                                                                                                          1134 AATCITCCGGTAATGGAGTTCTCCACTAGGTTGCGTATCGCCTTAGGTGCTGCGAAAGGA 1193
                                                                                                                                                                                                                                                                1490
                                                                                                                                                                                                                                                                                                                                               1270 GCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCT 1329
                                                                                                                                                                                                                                                                                                                                                                                                   1389
                                                                                                                                                                                                                                                                                                                                                                                                                                             1390 GIGCITITGGAGCICATTACTGGACGTCGACCGGIIGATGCCAACAATGICTATGTAGAT 1449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGTCAAAGCAATGTATACAGCTCATACGGAGGAAGCACCGATTATGACTGGAGCCAGTAC 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1731 GGACACAGTAACGTTTACGGGTCATTGGGAGCAAGCTCGGATTATAGTCAGACATCTTAC 1790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATGAAGACATGAAGAAGTTTAGGAAAATGGCACTTGGAACTCAAGAGTACAACGCCACG 1809
                    1374 CCAGANTATGCTTCAAGCGGTAAATTAACCGAGAAATCCGATGTTTTCTCTTACGGAGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1450 GACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1570 GITGCTIGTGCTGCGCTTGTGTTCGCCATTCAGCTCGCCGCAGACCTCGCATGAGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGCGGGTTCGGTTACGTGCACAAAGGTGTGGTTGCCTAGTGGGAAAGAAGTTGCTGAAG
                                                                                                                                                                                                                                                   CTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACGTGATATCAAGGCTTCA
                                                                                                                                                                                                                                                                                                  AACAIATIGAIAGAITICAAGITIGAAGCIAAGGITGCIGAITITIGGICIIGCIAAGAIT
                                                                                                                                                                                                                                                                                                                                                             1330 CCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1510 GAGGGTTTAGCTGATGCAAAGATGAATAATGGGTATGACAGAGAGGAGATGGCTCGCATG
                                                       CAGTTGAAAGTTGGGAGTGGTCAGGGAGGAGGGAGTTTTCAGGCAGAGGTTGAGATCATC
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PLN 27-DEC-2000

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DNA

79706 bp

AB020746

RESULT 11 AB020746 LOCUS

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Institute, Department of Plaint Gene Research; 1532.3, Kana, Kisaraau, Chiba 222-0812, Japan (E-mail:ynakamu@kazusa.or.jp, Tel:81-438-52-394)

Address for correspondence: Kaos@kazusa.or.jp
Roor the latest information on amortation of this clone, please see http://www.kazusa.or.jp/kaos/cgi-bin/agd_graph.cgi?c=MoB24 Genes with similarity to profeins in the databases are described in protein similarity to profeins in the databases are described in protein similarity are described as 'unknown protein.'
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory, Http://compbio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://compio.ornl.gov/Grail-1.3/), GENSCAN (Chris Burge, MIT, http://compio.alcorreleduce.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude.clude
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4757. .5179,5354. .5548,5693. .5970,6088. .6114,6297. .6496,
6601. .6648,6743. .6776,6882. .7013,7464. .7559,7677. .7743,
8162. .8217,8290. .8385,8470. .8998,9122. .9462))
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Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the 4,251,695 bp regions covered by 90 Pl. TAC
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This sequence may not be the entire insert of this clone. It may be shorter because we remove overlaps between neighboring submissions. The 5' clone is MXP5 and the 3' clone is MXP5 and clone is MXP5 and clone is MXP2 and clone is 
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VEGEEEDPQGGYIRGNERFQKRQKPNKVYSGFEFAGPSDAKVAYDWRBQEAFVLLEVW
GDRFLQLGRRSLRNEDWNFVAEKVSEELRMEKSETQCRRMIDDLKRKYRKEKIKVEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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GDSEEEEDEDDEVETERKKVNDAASYKMLADSVERFGKVYEKWEKSKKEQMKELEKMR
ADFQRDLELQKKQIVDRAQSETARLREEEENHHGGDDDESEEDEEMENDSDVNLSDE"
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Direct Submission
Submitted (03-DEC-1998) Yasukazu Nakamura, Kazusa DNA Research
Arabidopsis thaliana genomic DNA, chromosome 3, Pl clone: MOB24.
AB020746 BA000014
AB020746.1 GI:3985949
                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (strain:Columbia) DNA, clone_lib:Mitsui Pl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/product="DNA repair protein Muts"
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/organism="Arabidopsis thaliana"
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/db_xref="G1:9294038".
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2398. .3399
/note="gene_id:MCB24.1
unknown protein"
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DNA Res. 7 (3), 217-221 (2000)
20363099
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/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                               clone:MOB24.
Arabidopsis thaliana
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/evidence=not_experimental
/protein_id="BAB02001.1"
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STIDAQIEGPEDTVYANGIFNIKIQIPERYPFQPPIVSFATPIYHPNIDNSGRICLDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDGNGKRKAVVGFGEĞASFGNDGIKRSRKKLSIALPSQSQKKDLGGEBELITRGVSAAĞ
KENKKPULNOKKLSIGIKQPCRUTLASFRTSAAKSDNNKLSRKLSLRSPLGELNBVSK
PEVLAQTDAKLLEMNQNEDARSIRGEFENSVLEETSMAESIVVLDSEDSGQEEEFRVSS
SRSRLSLAKRRVLKCRP"
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AIPTYHLHHATPLWKSSITWLLRPOSKYEPPTYRFETSLSRAFILTOAMSHGETLLWD
TSLFGLTRILMFSSSASHGONQOTSTFPSPEMDASLSSSPYNGRHHHDLHLSEGKL
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TNHNELVLIWLHKNSLRTLPLVSSRIFVTGFICKNNGIMFPTPTSRWCDLCHPSATI
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TERRGODYQREPNISHRYPLITEKROKKENIIKESIBULQSIGKNGIMASSPWEDDYR
SFENILDLTPIVHLGDEQLQPLLIVVSRTGALEPYSTSSRLIFYNNLLSIDSFVED
PSTTRDLTCAIMPZSLMIKALMNFMSFHIITHILVLGNASFNYVLNFVIFESILLIFV
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/db_xref="61:929404"
/t=anslation="weddwswnnnnvylapfivkircmvndpstdwlitwepahnsf
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KISTYVEDPDLLPRAMIEKRETKOOOGVSDKKKRRYNGSTVASBEEFFEBEGRYFRV
MSSZPEPSTENLYRNHESDGMIVPHTGOOFSIETGLIVAKSBEEFFBEBGRYFRY
FYSLPEPSTVAGGGGGGGGGSIGERIKKRRYNGSTVASBESTSSISSITS
TPSLPEPSVAGGGGGGGGSIGERRYKETATFGGVVESNPPTTPPPYPPSEIRRGFF
COMPLEMENT (10in (37054. 37590.37670. 37809,37894. 38197,38289. 38398,38486. 38584,38662. 38772,39019. 39066,
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EKYAKVKADGCSTSIQIKNSGDEKSGESGNSVKLKLITVESSLSIAHTVKRETAGRDEQ
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/note="contains similarity to heat shock transcription
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/note="contains similarity to ubiquitin conjugating
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Pred. No. 1.3e-79;
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/note="emb|CAB79573.1
gene_id:MOB24.8
similar to unknown protein"
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/note="gene_id:MOB24.10
unknown protein"
                                                                                    gene_id:MOB24.7"
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IKELOKCSTYGFAFVDCAALREWGSISDDASCAALGALLMOVSFKEVLIDSK

GLSREOKALEKYTTGGSTAVOLAPVEVONDOTDAAGYRNITESOTFRGSESSWCA

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VOKITEWPRYPEIMFAKTVAPRAAGCTWYVKRAEOTSLEALFYAHLGKRAGTPDGYL
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IFVNCYFGFDLDCPYGGYKMSGNCRESGNDALDNYLQTKSVYPRLHNSPWM"
COODLEMPT (10in (19742. . . 19933, 20400. . 20657))
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FSPWKSPLPPPMPYDPPEEEEEEEKKEEETEDDPEKEDEDQPDNRS"
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ETRSAHPRYTSKHMACAFKSRBDYQPRGCDQDLWFLYRLTEGACPESYGLQVALMAGI
PNOVVETASGAAQAMKSIGENFKSSELRSEFSSLHEDWLKSLVGISRVAHNNAPIGE
DDYDTIFCLHHEIKSSTVPK*
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VKVDDRDCSGERSREDVVPLNDSSLCMKANDVIPQFRSNNGKTQERNHAFSFSGRAEL
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CGEKKEVNEGTKFEWLESSRIRDANRRRPDDPLYDRKTIHIPPDVFKKMSASQKQYWS
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complement(join(25945. .26640,26714. .26824,26914. .27012,
27119. .27224,27291. .27360,27436. .27583))
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/product="ethylene-responsive transcriptional
coactivator like protein"
/db_xref="01:9294040"
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/product="aldehyde dehydrogenase"
/protein_id="BAB01998.1"
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/note="gene_id:MOB24.6
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223 CTTCCTCAGCCGTCTCCACCTCCAACTACGCCGGATCTCCACCGGCACTGTTACT 282 	283 CCTCCTACTCGAAACCCTCCACGACCACGACCACGTCCAATCCTTCACGCGAA 342	52135 ACTCCTAGAACTCCAACAACACTAAACGCGCCGCCGTCTGATTCTTCCGATGGATTG 52194 403 TCAACAGGGTGGTGGTGGCAACGACGAGGAGTCGCTCGTGATAGTGACT 462	SILS ICIACCOGAGIIGIGGIAGGAAICGCCATIGGAGGAGICGCIATTCTTGTTAIACTGACT 52254  463 CTGATTGCCTCTGTAAGAAGAAGACGACGAGAGACGAAGAAGATGCTTAC 516	GGTCCCAAGGTCCCAAGGTAAAGTTCAAGTTCAAGTTCAAGTTCAAGTTCAAGTG			52455 AIRCHIGAITAIGEATTAICIGITAAAGAGATTACCETTGGAAAAGITTCAAACT 52494 549		644 CTAAGGCTCCATCTCCACCAGGCAACCTCCTCCACCTCCACCAGGGCTTTCATGA 700	701 SCAGCAGGGGGGTCCGACTACTCGGACCGTCCAGTTCTTCCTCCACGGGTCC 760 [	751 TTGTGTTAGGCTTCTCCAAAAGCACTTTCACATACGAGGAGCTAGGTAGAGCCACCAATG 820 	821 GTTTCTCCGAGGCGAACTTGTTAGGACAAGGCGGGTTCGGTTACGTGCACAAAGGTGTGT 880   1111   1	881 TGCCTAGTGGGAAAGAAGTTGCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAA 940 	941 GGGAGTITCAGGCAGAGGITGAGAICATCAGCAGAGTITCACCACAGGCAICIGGIGICIC 1000 	1603 TIGITGETATIGCATCGCGGTGCCAAAAGATIGCTTGTCTATGAGTTTGTTCCTAACA 1060 	
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Rosidae; eurosids II; Brassicales; Brassicae 1 (bases i to 2104) Goring, D. and Silva, N. Proline-rich extensin-like receptor kinases Patent: WO 0114563-A 9 01-MAR-2001; Goring, Daphne (CA); Silva, Nancy (CA) Location/Qualifiers

AUTHORS REFERENCE

JOURNAL PEATURES

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           1158 TTTGGATTGGCCTACAAGAGATGCATTGGGATCAGCTAGAGGCCTTGCATATTT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Iracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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AX088884 2104 bp Sequence 9 from Patent W00114563

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 13 AX088884 LOCUS

13

GI:13397647

Arabidopsis thaliana

ORGANISM

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Query Match   21.3%;   Score 413.6;   DB 6;   Length 2196;	1244 CGGTGAAGCAGCTGAAGATTGGGGAAAGAGAATTCCAGGCTGAGGTTG 13 1244 CGGTGAAGCAGCTGAAGATTCCAGGGAAAGAGAATTCCAGGCTGAGGTTG 13 1262 AGATCATCAGAGGTTCACCACAGGCATCTGTTGTTTTTTGATTTTTTTT	OY 1142 CTAAAGGACTTCTTATCTTCATGAAGATTGCAAATCCTAAAATCATCACGGGATATCA 1201	1373 TTTTCTCATTTGGGGTTGTGCTTTTGGAGCTCATTACTGGACCTCGACCGTTGATGCCA	Db 1904 CTCAGARGCAAACHTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
1488   AGCAICTGAGCAAGGAGACTTTGAGGGGTTAGCTGATGCAAGGTGAATAATGGGTATGA	1695 AAGCAATGIALACAGTCATAGGGGGGGGGGTTATGACTGGGGGGGGTGATGATGATTGAT	Db 2025 GAATAGAGGCTCAATGAA 2042  RESJLT 14  AX08888 LOCUS AX088888 LOCUS DEFINITION SEQUENCE 13 from Patent WO0114563.  ACCESSION AX088889.1 GI:13397651  KEYWORDS SOURCE CREAKISM Arabidopsis thaliana CREAKISM Arabidopsis thaliana Enkaryota; Viridiplantae; Streptop;yta; Embryophyta; Tracheophyta; Spermatophyta; Windiplantae; Streptop;yta; Embryophyta; Core endicots; Rosidae; eurosids 11; Brassicaceae; Arabidopsis.	REFERENCE 1 (bases 1 to 2196)  AUTHORS Goring, D. and Silva, N. TILLE Proline-rich extensin-like receptor kinases JOURNAL Patent: WO 0114563-A 13 01-MAR-2001; Goring, Daphne (CA); Silva, Nancy (CA) FEATURES 1. 2196  CDS 1. 2196  Abarref="taxon:3702"  Coson:sme"Arabidopsis thaliana"  Abarref="taxon:3702"  Coson:start="taxon:3702"  Abarref="taxon:3702"  Abarref="taxon:3702"  Abarref="taxon:3705"  Abarref="taxon:3705"	ACTAINED AND AND AND AND AND AND AND AND AND AN

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               1553 AGGAGAIGGCTCGCATGGTTGTTGTGCTGCGGCTTGTGTTCGCCATTCAGCTCGCCGCA
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OM nucleic - nucleic search, using sw model

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Perfect score:

US-10-086-464-1 1944 1 atgreeteggegeegtetee.....atagtggacettetetttaa 1944

Sequence:

Scoring table:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0

4370478 Total number of hits satisfying chosen parameters:

2i85239 seqs, 1125999159 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N\_Geneseq\_101002:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

AAF77094 standard; DNA; 1944 BP. (first entry) Brassica napus PERK1 DNA. 17-MAY-2001 AAF77094; RESULT 1 

Proline-rich extensim-like receptor kinase; PERK; resistance; plant; ds.

Brassica napus.

WO200114563-A1.

01-MAR-2001.

18-AUG-2000; 2000WO-CA00966.

99US-0149466. 99US-0159122. 19-AUG-1999; 13-OCT-1999;

(GORI/) GORING D. (SILV/) SILVA N.

Goring D, Silva N;

WPI; 2001-244305/25.

New proline-rich, extensin-like receptor kinase nucleic acids and

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polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding
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                   pathogen resistance
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1861 AGCAGGGGCCAAACCACACGAAATGGAGATGGGGAAGTTAAGAGAACCGGTCAG 1920
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    IIGATAGATTICAAGITTGAAGCTAAGGITGCIGATTTTGGTCTTGCTAAGATIGCTTCT 1275
                                                         GALACAAACACGCAIGTATCAACACGTGTGAIGGGAACCTTTGGGTACTTGGCTCCGGAA 1335
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                                                                                                                                                                                                   1516 TTAGCTGATGCAAAGATGAATAGTGGGTATGACAGAGGAGGAGAGAGGCTCGCATGGTTGCT
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946 TITCAGGCAGAGGIIGAGAICAICAGCAGAGIICACCACAGGCAICIGGIGICICITGII 1005
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DB 21; Length 1703; Indels

Score 215.8; DB 21; Pred. No. 1.6e-41; 0; Mismatches 287;

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                             1297 ACACGTGTGATGGGAACCTTTGGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTC 1356
                                                                                                                                                        1417 CGACCCGTTGATGCCAACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCA 1476
1357 ACGGAGAAGTCIGACGTTITCTCATTIGGCGTIGIGCITTIGGAGCTCATTACIGGACGT
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929 CIGTTAAC 937
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25 MAR. 1999;
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1038
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   1153 TCTIATCTTCATGRAGATTGCAATCCTAAAATCATTCACGTGATATCAAGGCTTCAAAC 1212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  616 CGACACAAGAATCTIGTTAGGCTTTTAGGGTATTGCGTGGAAGGTGCATACAGGATGCTC 675
                                                                                                                                                                                                                                                                                                                                                                  736 GICAGCCCGCTAACIIGGGATATACGIATGATATIAIACGGGGATGGCCAAAGGATIG 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               975
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                                                                                                                                                 799 GAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTGTTAGGACAAGGCGGGTTC
                                                                                                                                                                GGTTACGTGCACAAAGGTGTTGCCTAGTGGGAAAGAAGTTGCTGTGAAGCAGTTGAAA
                                                                                                                                                                                                                   919 GTTGGGAGTGGTCAGGGAGAGAGGGAGTTTCAGGCAGAGGTTGAGATCATCAGCAGAGTT
                                                                                                                                                                                                                                                                  CACCACAGGCATCTGGTGTTGGTTATTGCATCGCCGGTGCCAAAAGATGGTT
                                                                                                                                                                                                                                                                                                                                                 1039 GICTATGAGITTGTICCTAACAACAATCTCGAGC----TICACCTCCATGGCGAGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1213 ATAITGATAGAITICAAGIITGAAGCIAAGGITGCIGAITITIGGICTIGCIAAGAITGCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1273 TCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   916 GGGTCTGAGAGCAGTTAIGTGACTACTCGTGTGAGGAACTTTCGGTTATGTAGCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1333 GAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTTGTG
                                                                                                                             Gaps
                                                                                                   DB 21; Length 1419;
                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana DNA fragment SEQ ID NO: 37126
                                                                                                                            0; Mismatches 289;
                                                                                                   Score 204.6; DB 2
Pred. No. 6.9e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1453 AGCTTAGTTGACTGGGCACGACCATTGCT 1481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATCTAGTGGATTGGCTTAAATCAATGGT 1124
990S-0161359.
990S-0161360.
990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
                                                                                                   10.5%;
57.2%;
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                                                                                               Query Match 10.55
Best Local Similarity 57.27
Matches 394; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
28-0CT-1999;
28-0CT-1999;
29-0CT-1999;
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990S-0140823.
990S-0141287.
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990S-0141285.
990S-0142055.
990S-0142363.
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990S-014237.
990S-0144331.
990S-0144332.
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990S-0144334.
990S-0144332.
990S-0145086.
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990S-0145087.
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990S-0146386.
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990S-0147389.
990S-0147038.
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990S-0147303
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990S-0147416
990S-0147493
990S-0148171
990S-0148319
990S-014864
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990S-0145918.
990S-0145919.
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99US - 0149172
99US - 0149723
99US - 0149929
99US - 0149930
99US - 0149930
99US - 0150884
99US - 0151085
99US - 0151085
99US - 0151085
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99US-0151930.
99US-0152363.
28 - JUN - 1999;
29 - JUN - 1999;
01 - JUL - 1999;
01 - JUL - 1999;
02 - JUL - 1999;
08 - JUL - 1999;
09 - JUL - 1999;
12 - JUL - 1999;
13 - JUL - 1999;
14 - JUL - 1999;
                                                                                                                                       19-701-1999

19-701-1999

19-701-1999

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22-701-1999
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20-AUG-1999;
20-AUG-1999;
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23-AUG-1999;
25-AUG-1999;
26-AUG-1999;
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05-AUG-1999;
06-AUG-1999;
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02-AUG-1999
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13-AUG-1999
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16-AUG-1999
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18-AUG-1999;
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09-AUG-1999
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metabolic pathway; promoter; termination sequence; ss
                                                                              990S-0121825.
990S-0123180.
990S-01233180.
990S-0125784.
990S-0125784.
990S-0125784.
990S-0125785.
990S-01257462.
990S-0128144.
990S-0132484.
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990S-013446.
990S-013456.
990S-013465.
990S-013465.
990S-0139456.
990S-0139456.
                                                               25-FEB-2000; 2000EP-0301439
               Arabidopsis thaliana
                                                                              25-FEB-1999,
05-MAR-1999,
23-MAR-1999,
23-MAR-1999,
29-MAR-1999,
01-APR-1999,
06-APR-1999,
16-APR-1999,
16-APR-1999,
16-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
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18-JUN-1999;
18-JUN-1999;
                               EP1033405-A2
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23-JUN-1999;
24-JUN-1999;
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9-MAY-1999;
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                                                36-SEP-2000
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05-MAY-1999
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ATAITGATAGATITCAAGIITGAAGCIAAGGIIGCTGAITITGGICTTGCIAAGATIGCI 1272
                                                                                                                                 TCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACCTTTGGGTACTTGGCTCCG 1332
                                                                                                                                                                                                GAATACGCTGCAAGCGGAAAGCTCACGSAGAAGTCTGACGTTTTCTCATTTGGCGTTGTG 1392
                                                                                                                                                                                                                1393 CTTTTGGAGCTCATTACTGGACGTCGACCCGTTGATGCCAACAATGTCTATGTAGATGAC 1452
                                                                                                                                                                                                                                                                                             1054 ATCATGGAGATAATCACCGGAAGAATCCTGTCGATTATAGTCGACCTCAAGGAGGTG 1113
      1153 TCTTAICTTCATGAAGATTGCAATCCTAAAATCATTCACCGTGATATCAAGGCTTCAAAC 1212
                                      873
                                                                                                                                                   934 TTCTCCGAGAGCAGCTACGTGACAACCCGAGTAATGGGAACTTTTGGATATGTTGCGCCT 993
                                                                                                                                                                                                                                                                                                                          1453 ACCTTAGTTGACTGGCACGACCATTGCTT---AACCGAGCATCTGAGCAAGGAGAC 1506
                                                                                                                                                                                                                                                                                                                                           814 GCCIAICTGCATGAGGGTCTTGAACCGAAAGTCGTTCATCGGGACATAAAATCTAGTAAI
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990S-0123180.
990S-0123788.
990S-0125788.
990S-0126785.
990S-0127465.
990S-0127465.
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990S-0130891.
990S-0131449.
990S-013248
990S-0132485.
990S-0132486.
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990S-0134256.
990S-0134218.
990S-0134219.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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01-APR-1999
08-APR-1999
08-APR-1999
116-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
23-APR-1999
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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05-MAY-1999;
06-MAX-1999;
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30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GICIAIGAGIIIGIICCIAACAACAAICICGAGCIICACCICCAIGGCGAGGGACGGCCI 1098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACAA----TGGAATGGAGCACCAGAITGAAGAITGCTCTIGGATCTGCTAAAGGACTT 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              693
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAAGTCCGTTGACTTGGGATATTCGTATGAACATAATACTTTGCATGGCGAAAGGATTG 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574 AACAACAGGGTCAAGCTGAGAAGGAGTTTAGAGTGGAAGTGGAAGCTATCGGGCGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         634 AGGRIAAGAATCTCGTTAGGTATTAGGATACTGCGTCGAAGGAGCATACAGGATGCTC
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Pred. No. 1.5e-37;
0; Mismatches 300; Indels
                                                                                                                                                                                                                                                                                    9905-0159295
9905-0159329-
9905-0159330-
9905-0159330-
9905-0159330-
9905-0159638-
9905-0160767-
9905-0160768-
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9905-0153070.
9905-0153758.
9905-0154018.
9905-0154739.
9905-015486.
9905-0155486.
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990S-0155596.
990S-0157117.
990S-0157753.
990S-0157865.
990S-0158823.
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990S-0159293.
990S-0159294.
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99US-0161406.
99US-0161359.
99US-0161360.
99US-0161920.
99US-0161922.
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99US-0162142
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Best Local Similarity 56.9
Matches 408; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
26-0CT-1999;
                                              16 - SEP - 1999

20 - SEP - 1999

21 - SEP - 1999

24 - SEP - 1999

26 - SEP - 1999

27 - SEP - 1999

28 - SEP - 1999

29 - SEP - 1999

20 - OCT - 1999

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21 - OCT - 1999

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27 - OCT - 1999
10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
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protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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99US-0126264.
99US-0126785.
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99US-0134256.
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                                   Arabidopsis thaliana
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     979 CACCACAGGCATCTGGTGTCTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTT 1038
                                                                                                                                                                                                                                                                                                                      GTCTATGAGITTGTTCCTAACAACATCTCGAGCTTCACCTCCATGGCGAGGGACGGCCT 1098
                                                                                                                                                                                                                                                                                                                                                                  ACAA-----TGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTT 1152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1333 GAATACGCIGCAAGCGGAAAGCTCACGGAGAAGICTGACGTTTTCTCATTTGGCGTTGTG 1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1393 CTTTTGGAGCTCATTACTGGACGTCGACCCGTTGAIGCCAACAATGTCTATGTAGATGAC 1452
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                                                                                                                                                                                                                                                     574 AACAACAGGGTCAAGCTGAGAAGGAGTTTAGAGTGGAAGTGGAAGCTATCGGGCGTGTA 633
                                                                                                                                                                                                                                                                                                634 AGGCATAAGAATCTCGTTAGGCTATTAGGATACTGCGTCGAAGGAGCATACAGGATGCTC 693
                                                                                                                                                                                                                                                                                                                                            694 GIGTALGACIACGICGALAATGGCAACTIGGAGCAATGGAITCAIGGGALGITGGIGAI 753
                                                                                                                                                                                                                                                                                                                                                                                   1453 AGCTTAGTTGACTGGGCACGACCATTGCTT---AACCGAGCATCTGAGCAAGGAGAC 1506
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                                                                                                                                             799 GAGCIAGCIAGCCACCAAIGGTTTCTCCGAGGCGAACTTGTTAGGACAAGGCGGGTTC
                                                                                                                                                                                        GGTIACGTGCACAAAGGTGTTGCCTAGTGGGAAAGAAGTTGCTGTGAAGCTTGAAA
                                                                                                                                                                                                           514 GGGATTGITTATAGTGGGATTTTAACTGATGGAACTAAAGTCGCTGTCAAGAATCTGCTT
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                                                                                                    Length 1626;
                                                                                                                       0; Mismatches 300; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thallana DNA fragment SEQ ID NO: 48093.
                                                                                                   Score 199; DB 21;
Pred. No. 1.6e-37;
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 990S-0161406.
990S-0161359.
990S-0161360.
990S-0161361.
990S-0161992.
990S-0161993.
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                                                                                                                       408; Conservative
                                                                                                             Similarity
25-0Cz-1599;
26-0Cz-1599;
26-0CT-1599;
26-0CT-1599;
28-0CT-1599;
28-0CT-1599;
29-0CT-1599;
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9905-0141842

9905-0142154

9905-0142395

9905-0142396

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G----AGGGACGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTGGATCT 1140
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Pred. No. 4.1e-37;
0; Mismatches 268; Indels
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990S-0156459
990S-0157117
990S-0157753
990S-0157865
990S-015823
990S-0158362
990S-015933
990S-0159293
990S-0159294
990S-0159295
990S-0152363.
990S-0153070.
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99US-0162142.
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nes 374; Conserv
10.7 SEP 11999;
13. SEP 11999;
15. SEP 11999;
16. SEP 11999;
22. SEP 11999;
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24. SEP 11999;
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                                                                                                       TACTIGGCICCGGAATACGCIGCAAGCGGAAAGCICACGGAGAAGICIGACGIIIICICA 1380
                                                                                                                 1039 TACGTTGCTCCTGAATATGCAAACTCAGGGTTGTTAAATGAAAGAGTGATGTCTACAGG 1098
              978
                                               1381 TTTGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCCGTTGAT 1428
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1180 AGACCGCCTGGCGAGATGAACTTAGTGGATTGGTTCAAAGGAATGGTTGCAAGTAGACGT 1239
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                                       940 GATGTGAAATCTAGTAACATCTTGCTCGATAAGAAATGGAACGCGAAAGTGTCTGATTTT
                         GGTCTTGCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGAACC
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19-APR-1999;
21-APR-1999;
23-APR-1999;
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05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
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14-MAY-1999;
18-MAY-1999;
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06-APR-1999;
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30-APR-1999;
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99US-0160814.
99US-0160815.
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28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 03-AUG-1999; 04-AUG-1999; 04-AUG-1999; 05-AUG-1999; 05-AUG-1999; 06-AUG-1999;	06-AUG-1999; 09-AUG-1999; 09-AUG-1999; 11-AUG-1999; 13-AUG-1999; 13-AUG-1999; 13-AUG-1999; 17-AUG-1999; 17-AUG-1999; 20-AUG-1999; 20-AUG-1999; 20-AUG-1999;	23 AUG-1999; 25 AUG-1999; 25 AUG-1999; 27 AUG-1999; 27 AUG-1999; 30 AUG-1999; 31 AUG-1999; 07 SEP-1999; 10 SEP-1999; 11 SEP-1999; 15 SEP-1999; 16 SEP-1999; 16 SEP-1999; 16 SEP-1999; 17 SEP-1999;	22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 26-SEP-1999; 04-OCT-1999; 06-OCT-1999; 06-OCT-1999; 07-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999;	14 - OCT - 1999 14 - OCT - 1999 14 - OCT - 1999 18 - OCT - 1999 21 - OCT - 1999 21 - OCT - 1999 21 - OCT - 1999 21 - OCT - 1999 22 - OCT - 1999 22 - OCT - 1999 25 - OCT - 1999 25 - OCT - 1999 26 - OCT - 1999 27 - OCT - 1999 28 - OCT - 1999 29 - OCT - 1999 20 - OCT - 1999 20 - OCT - 1999 21 - OCT - 1999 22 - OCT - 1999 23 - OCT - 1999 24 - OCT - 1999 25 - OCT - 1999 26 - OCT - 1999 27 - OCT - 1999 28 - OCT - 1999 29 - OCT - 1999 20 - OCT - 1999 20 - OCT - 1999 21 - OCT - 1999 22 - OCT - 1999 23 - OCT - 1999 24 - OCT - 1999 25 - OCT - 1999 26 - OCT - 1999 27 - OCT - 1999 28 - OCT - 1999 29 - OCT - 1999 20 - OCT - 1999 20 - OCT - 1999 21 - OCT - 1999 22 - OCT - 1999 23 - OCT - 1999 24 - OCT - 1999 25 - OCT - 1999 26 - OCT - 1999 27 - OCT - 1999 28 - OCT - 1999 29 - OCT - 1999 20 - OCT - 1999 21 - OCT - 1999 22 - OCT - 1999 23 - OCT - 1999 24 - OCT - 1999 25 - OCT - 1999 26 - OCT - 1999 27 - OCT - 1999 28 - OCT - 1999 29 - OCT - 1999 20 - O
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Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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990S-0132484.
990S-0132485.
990S-0132486.
990S-0132487.
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99US-0126785.
99US-0127462.
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99US-0131449.
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990S-0134780
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990S-0136782.
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990S-0137724.
990S-0138094.
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99US-0123548
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99US-0130510
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                                                  Arabidopsis thaliana
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01-APR-1999
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08-APR-1999
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30-APR-1999,
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04-MAY-1999;
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11-MAY-1999;
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18-MAY-1999;
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01-JUN-1999;
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21-JUN-1999;
22-JUN-1999;
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06-APR-19
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       CACCACAGGCATCTGGTGTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTT 1038
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Pred. No. 1.5e-36;
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         990S-0161361.
990S-0161920.
990S-0161992.
990S-0161993.
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55.5%;
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26-OCT-1999;
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Matches 401;
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9US-0140353 9US-0140354 9US-0140802 9US-0140801 9US-0141287 9US-0141287 9US-01421842 9US-01421842 9US-0142180 9US-0142180 9US-0142803 9US-0142803 9US-0142803	90S-0144086 90S-0144325 90S-0144333 90S-0144333 90S-0144333 90S-0144335 90S-0144335 90S-0144635 90S-0144635 90S-0145086 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087 90S-0145087	99US-0145388. 99US-0145389. 99US-0147204. 99US-0147204. 99US-0147192. 99US-0147493. 99US-0147493. 99US-0147493. 99US-0147493. 99US-0147493. 99US-0148319. 99US-0148319. 99US-0148319. 99US-0149426. 99US-0149426. 99US-0149426. 99US-0149920. 99US-0149920. 99US-0149920. 99US-0149920. 99US-0149930. 99US-015066. 99US-015066.
3.00x-1999 3.00x-1999 4.00x-1999 9.00x-1999 9.00x-1999 1.00x-1999 1.00x-1999 9.00x-1999 9.00x-1999 9.00x-1999 3.00x-1999 3.00x-1999 3.00x-1999 3.00x-1999	6 - UII - 1599 9 - UII - 1999	0.2-AuG-1999; 0.3-AuG-1999; 0.4-AuG-1999; 0.4-AuG-1999; 0.5-AuG-1999; 0.5-AuG-1999; 0.5-AuG-1999; 0.5-AuG-1999; 11-AuG-1999; 12-AuG-1999; 13-AuG-1999; 13-AuG-1999; 17-AuG-1999; 23-AuG-1999; 23-AuG-1999; 21-AuG-1999;
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	Gaps	ACITGI           ATTIGC
	1674; 9;	GGCGAL         AGTTAL
	Length	TTCTCCGP          TTCCGGGA
	Score 194.6; DB 21; Pred. No. 1.8e-36; ; Mismatches 319;	GCACTTTCACATACGAGGAGGTAGCTAGAGCCACCAATGGTTTCTCCGAGGGGAACTTGT 
990x-0151336. 990x-0151336. 990x-01513370. 990x-0153770. 990x-0153779. 990x-0154739. 990x-0154739. 990x-0155559. 990x-0155659. 990x-0155659. 990x-0155659. 990x-0155631. 990x-0155631. 990x-0159231. 990x-0159231. 990x-0159331. 990x-0159331. 990x-0159331. 990x-0159331. 990x-0159331. 990x-0159331. 990x-0159331. 990x-0159631. 990x-0160981. 990x-0160980.	0%; 9%; 0	ZATACGAGGAGCTZ                     CGTTCAAGGAGTTZ
	Similarity 55.5; Conservative	CTTTCAC          SCTTCAC
31-AUG-1999; 07 - SEP-1999; 10 - SEP-1999; 110 - SEP-1999; 12 - SEP-1999; 13 - SEP-1999; 24 - SEP-1999; 25 - SEP-1999; 26 - SEP-1999; 27 - SEP-1999; 28 - SEP-1999; 29 - SEP-1999; 20 - OCT-1999; 21 - OCT-1999; 22 - OCT-1999; 23 - SEP-1999; 24 - SEP-1999; 25 - OCT-1999; 26 - OCT-1999; 27 - OCT-1999; 28 - OCT-1999; 28 - OCT-1999; 29 - OCT-1999; 20 - OCT-1999; 21 - OCT-1999; 22 - OCT-1999; 23 - OCT-1999; 24 - OCT-1999; 25 - OCT-1999; 26 - OCT-1999; 27 - OCT-1999; 28 - OCT-1999; 29 - OCT-1999; 21 - OCT-1999; 22 - OCT-1999; 23 - OCT-1999; 24 - OCT-1999; 25 - OCT-1999; 26 - OCT-1999; 27 - OCT-1999; 28 - OCT-1999; 29 - OCT-1999; 29 - OCT-1999; 20 - OCT-1999;	Query Match Best Local Simil Matches 415; (	782 GCA(   1 553 GGA(
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1080 ----CCATGGCGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCTTG 1135

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                                                                                   AIATCAAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTG 1255
                                                                                                                                     GTCTTGCTAAGATTGCTTCTGATACAAAC---ACGCATGTATCAACACGTGTGATGGGAA 1312
                                                                                                                                                                                                     GTCAAAAGCAAGGGGAGGAGAATCTTGTTACTTGGTCAGGTCCATACCTCAAGGATCAGA 1272
                 912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:886.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
plant cell signalling; modulation; transgenic plant; pathogen; growth;
environmental change; development; cell proliferation; differentiation;
elongation; survival; disease resistance; nutrient metabolism; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disted polynucleotide encoding a polypeptide involved in cell gnaling used for generating transgenic plants with modified responses external signals -
GATCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCGTG
                                                           GIGCAGCICGAGGAATAGAGIAICITCACTGCACAGCIAACCCGCCAGIGAITIAACCGIG
                                                                                                         ATTIGAAATCCGCAAACATATTGTTAGATAAAGAGTICAGTCCAAAACTCTCGGATTTCG
                                                                                                                                                             GATTGGCGAAACTCGGTCCAGTTGGTGATCGAACTCATGTATCGACTCGTGTCATGGGAA
                                                                                                                                                                                     CCTTTGGGTACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACG
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AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Bucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences

Claim 1: Page 438-439; 527pp; English.

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are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance modifications can be used to delay senescence in selected cell types or ergans providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease sizanching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers.
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                                                                                                                                                                                                                                                                                                                       DB 21; Length 3108;
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                                                                                                                                                                                                                                                                            Sequence 3108 BP; 778 A; 708 C; 719 G; 903 T; 0 other;
                                                                                                                                                                                                                                                                                                                     Score 192.4; DB 21;
Pred. No. 7.6e-36;
0; Mismatches 356;
                                                                                                                                                                                                                                                                                                                   9.9%;
                                                                                                                                                                                                                                                                                                                                                    Matches 419; Conservative
                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  920
                                                                                                                                                                                                                                                                        New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTATGTTCATAAAGGAGTTCTGCCTAGTGGCAAAGAAGTTGCAGTGAAGAGTCTTAAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                       The present invention relates to proline-rich extensin-like receptor kinase (PERR). The PERR nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide function directly.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22; Length 2820;
                                                                        Proline-rich extensin-like receptor kinase; PERK; resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2820 BP; 819 A; 629 C; 577 G; 795 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 192.2; DB 2
Pred. No. 8.2e-36;
AAF77097 standard; DNA; 2820 BP.
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99US-0159122
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                                                                                                                                                                                                                                                                                                                      Examples; Fig 13; 91pp;
                                                                                                                                                                                                                                                                                                     pathogen resistance
                                                                                                    Arabidopsis thaliana.
                                                                                                                                                                                                                                                       WPI; 2001-244305/25.
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es 272; Conserv
                                                                                                                                                                                                         (GORI/) GORING D. (SILV/) SILVA N.
                                                                                                                       WO200114563-A1.
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13-OCT-1599;
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                                                       Arabidopsis
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                                                                                   plant; ds.
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                  AAF77097
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding
  CCACAGGCATCTGGTGTCTTGTTGGTTATTGCATCGCCGGTGCCAAAGATTGCTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         790 ACATACGAGGAGCTAGCTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTGTTAGGACAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Proline-rich extensin-like receptor kinase; PERK; resistance;
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                                                                                                             Indels
                                                                                      1041 CTATGAGTTTGTTCCTAACAACAATCTCGAGCTTCACCTCCATGG
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Pred. No. 8.8e-36;
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                                                                                                                                                                                                                                                                                                                                                                             gene #2.
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255; Conserv
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13-OCT-1999;
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23-JUL-1999
  961 GGAGGAITIGGGTATGTCCATAAAGGAGTCTTGCCTAGCGGGAAAGAAGTAGCAGTTAAG 1020
                 910 CAGTTGAAAGTTGGGAGTGGTCAGGGAGAGGGAGTTTCAGGCAGAGGTTGAGATCATC
                                                                                                                                                                                                                            Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                            Arabidopsis thaliana DNA fragment SEQ ID NO: 65175.
                                                                                                                                                     AAC50527 standard; DNR; 1848 BP
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Sequence 672, App
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Sequence 52, Appl
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US-10-988-484-1911
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Maximum Match 1008
Listing first 45 summaries
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seq length: 200000000
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Sequence 4, Appli Sequence 9, Appli Sequence 7, Appli Sequence 159, Appli Sequence 799, Appl Sequence 51, Appl Sequence 461, Appl Sequence 461, Appl Sequence 262, Appli Sequence 262, Appli Sequence 262, Appli Sequence 2569, Ap Sequence 1181, Ap Sequence 1179, Ap Sequence 1750, Ap Sequence 1750, App Sequence 888, App Sequence 1414, App Sequence 1416, Ap Sequence 1270, Ap Sequence 1270, Ap Sequence 1270, Ap Sequence 2579, Ap Sequence 2579, Ap Sequence 2579, Ap US-09-934-948-91 US-10-101-464A-461 US-10-101-464A-461 US-09-938-842A-575 US-09-938-842A-159 US-09-938-842A-1181 US-09-938-842A-1181 US-09-938-842A-1175 US-09-938-842A-1175 US-09-938-842A-1149 US-09-938-842A-11496 US-09-938-842A-11496 US-09-938-842A-1270 US-09-938-842A-1270 US-09-938-842A-1270 US-09-938-842A-1270 US-09-938-842A-1270 US-09-938-842A-1270 US-09-938-842A-1270 US-09-938-842A-1270 US-09-938-842A-1270 US-10-101-464A-4
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## ALIGNMENTS

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                                Sequence 1, Application US/10086464

Publication No. US2020199218A1

GENERAL INFORMATION:

APPLICANT: GORING, Daphne R. et al.

TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES;

FILE REFERENCE: P. 25, 762-A USA

CURRENT FILING DATE: 2002-02-8

PRIOR APPLICATION NUMBER: US 10/069,364

PRIOR PLING DATE: 2002-02-19

PRIOR PLING DATE: 2000-08-18

PRIOR PLING DATE: 1099-08-19

PRIOR PLING DATE: 1999-08-19

PRIOR APPLICATION NUMBER: US 60/149,466

PRIOR PLING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

PRIOR FILING DATE: 1999-08-19

NUMBER OF SEQ ID NOS: 27

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 1

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121 CCATCCACTATECCGACATCTCCTCCTTCTTCTCGCTCTACACCTTCTGCTCCTCT 180

us-10-086-464-1.rnpb

1201 AAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGGTTGCTGATTTTGGTCTT   09	1441	Dy 1561 GCTCGCARGGTTGCTGCGGGTTGTTGTTGTTCAGCTCGCCGCAGACCTCGC [IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	OY 1681 ATGAGACCAGGTCAAAGCAATGTATACAGCTCATACGGAGGAGCACCGATTATGACTCG	1801	QY 1861 ACCAGGAGGCCAAACACGGAAATGGAGATGAGGAAGTTAAGAAACGGGTAG	DD 1921 GGTTATAGTGGACCTTCTCTTTAA 1944 RESULT 2	US-10-086-464-3 ; Sequence 3, Application US/10086464 ; Publication No. US20020199218A1 ; GENERAL INFORMATION: ; APPLICANT: GORING, Daphne R. et al. ; TITLE OF INVENTION: ; TIT	CURRENT APPLICATION NUMBER: US/10/086,464 CURRENT FILING DATE: 2002-02-28 PROR APPLICATION NUMBER: US 10/069,304	PRIOR FILLING DATE: JOUZ-02-19  PRIOR PELLOATION NUMBER: PCI/CA00/00966  PRIOR FILLING DATE: 2000-08-18  PRIOR APPLICATION NUMBER: US 60/149,466	; PRIOR FILING DATE: 1959-08-19; PRIOR APPLICATION WUGER: US 60/159,122; PRIOR FILING DATE: 1959-10-13; NUMBER OF SEQ ID NOS: 27	; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 3 ; LENGTH: 2189
THE COLUMN ACCOUNTS A		CY 481 AAGAAGAAACGAGAGAGAGAGAGAGATTACTTATGTTCCTCGCCACCTCCTCT 540	QY         501 ACACCACCGICAGAICATGTCGTGACGTCACTACCACCACCACCACCATCGTCCA 660           III:	CAAA CAAA	CTTG		Db 901 GCTGTGAAGCAGTGAAGAGTGGGAGAGGGGGGGGGGGGG	09 1021 GGTGCCAAAAGATTGCTTGTCTATGTTCCTAACAACAATCTCGAGCTTCACCIC 1080 [11] [1] [1] [1] [1] [1] [1] [1] [1] [1	Oy 1081 CAIGGCGAGGACGACTACAAIGGAAIGGAGCACCAGAIIGAAGAIIGGAAICI 1140	OY 1141 GCTAAAGGACTTTCTTATCTTCATGAAGATTGCAAAATCATTCACGGTGATATC 1200	OY 1201 AAGGCTTCAAACATATTGATTTCAAGTTTGAAGCTAAGGTTGCTGATTTTGGTCTT 1260

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US-10-086-464-3
TYPE: DNA ORGANISM: Brassica
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TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES;
FILE REFERENCE: P 25,762-A USA;
CURRENT APPLICATION NUMBER: US 10/069,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: DCT/CA00/00966
PRIOR FILLING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: DCT/CA00/00966
PRIOR FILLING DATE: 2006-08-19
PRIOR PILLING DATE: 1999-08-19
PRIOR FILLING DATE: 1999-10-13
PRIOR PELLING DATE: 1999-10-13
SPRIOR FILLING DATE: 1999-10-13
SOFTWARE: PARENTIN VOR: 2.1
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; ORGANISM: Arabidopsis thaliana
US-10-086-464-9
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                                                          JENERAL INCOMENTATION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REPERENCE: P. 25,762-A. USA
CURRENT APPLICATION NUMBER: US.10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: ECT/CA00/00966
PRIOR APPLICATION NUMBER: ECT/CA00/00966
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.1
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               Sequence 10, Application US/10086464 Publication No. US20020199218A1 GENERAL INFORMATION:
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Matches 747; Conserv
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GORING, Daphne R. et al.

TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

FILE REFERENCE: P 25,762-A USA

CURRENT APPLICATION NUMBER: US/10/086,464

CURRENT FILING DATE: 2002-02-28

PRIOR RPLICATION NUMBER: US 10/069,304

PRIOR RILING DATE: 2002-02-8

PRIOR PILING DATE: 2000-09-18

PRIOR PLILING DATE: 1999-00-18

PRIOR PLILING DATE: 1999-08-19

PRIOR PLILING DATE: 1999-10-13

PRIOR PLILING DATE: 1999-10-13

**NUMBER OF SEQ ID NOS: 27

**SOFFWARE: PATCHIN NUMBER: US 50/159,122

**PRIOR PLILING DATE: 1999-10-13

**NUMBER OF SEQ ID NOS: 27

**SOFFWARE: PATCHIN VET. 2.1
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Best Local Similarity 61.8%;
Matches 790; Conservative
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US-10-086-464-13
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Score 427.2; DB 9; Pred. No. 1.3e-113; 0; Mismatches 413;

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TGATITIGGTCTTGCTAAGATIGCTTCTGATACAAACACGCATGTATCAACACGTGTGAT

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RESULT 5 US-10-086-464-13

Sequence 13, Application US/10086464

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                                                                                                                                 TGCCAACAATGTCTATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCG 1487
                                                                         774 TCCACAGCAACTGTGTGTGTCTCACAGTGATGCTTCCAACTTAACGGTGGAACTGC
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   Pred. No. 1.3e-113;
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         GGGAACCTTTGGGTACTTGGCTCCGGAATACGCTGCAAGGGGGAAAGCTCACGGAGAAGTC
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TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REFERENCE: P 25,762-A 0SA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-29
PRIOR PLILING DATE: 2002-02-19
PRIOR PLILING DATE: 2002-02-19
PRIOR PLILING DATE: 2000-08-18
PRIOR PLILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/149,466
PRIOR PLILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
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US-10-086-464-12
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LENGTH: 2104
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GENERAL INVOCATION:
GENERAL INVOCATION:
TITLE OF INVENTION: PROLINE-RICH EXTERSIN-LIKE RECEPTOR KINASES:
FILE REFERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/006,454
CURRENT FILING DAIE: 2002-02-28
PRIOR APPLICATION NUMBER: DCI/CA00/00966
PRIOR APPLICATION NUMBER: PCI/CA00/00966
PRIOR APPLICATION NUMBER: PCI/CA00/00966
PRIOR FILING DATE: 2000-08-18
PRIOR PLILNG DATE: 1999-08-19
PRIOR FILING DATE: 1999-10-13
PRIOR PLILNG DATE: 1999-10-13
SPRIOR FILING DATE: 1999-10-13
SEQ ID NOS: 27
SEQ ID NOS: 27
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Pred. No. 1.3e-109;
0; Mismatches 289;
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Best Local Similarity 67.0%;
Matches 606; Conservative
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US-10-086-464-15
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TITLE OF INVENTION: PROLINE-RICE EXTENSIN-LIKE RECEPTOR KINASES
FILE REFERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 12/069,304
PRIOR FILING DATE: 2002-02-19
PRIOR FILING DATE: 2000-02-19
PRIOR PRIOR APPLICATION NUMBER: US 60/149,466
PRIOR FILING DATE: 1999-08-19
PRIOR APPLICATION NUMBER: US 60/159,122
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
PRIOR FILING DATE: 1999-08-19
SPRIOR FILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 27
LENGTH: 2196
LENGTH: 2196
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Pred. No. 1.2e-109;
0; Mismatches 289;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/10086464 Publication No. US20020199218A1 GENERAL INFORMATION:
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CRGANISM: Arabidopsis thaliana
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al Similarity 67.0%;
606; Conservative (
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US-10-086-464-16
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US-10-086-464-16
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US-10-066-464-7
Sequence 7, Application US/10086464
Fublication No. US20020199218A1
GENERAL INFORMATION:
APPLICANT: GORING, Daphne R. et al.
TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
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Pred. No. 3.6e-78;
0; Mismatches 344;
FILE REFERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR PILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: PCT/CA00/00966
PRIOR PILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/149,466
PRIOR PILING DATE: 1999-08-19
PRIOR PILING DATE: 1999-10-13
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN VET: 2.1
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59.1%;
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Best Local Similarity 59.1
Matches 644; Conservative
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LOCATION: (1)
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
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             CAGCITAGITGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGACTTTGA 1511
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                                                                             Sequence 6, Application US/10086464

Publication No. US2020199218A1

GENERAL INFORMATION:

APPLICANT: GORING, Dapine R. et al.

IIILE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

FILE REPRENCE: P 25,782-A USA

CURRENT APPLICATION NUMBER: US/10/086,464

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 10/069,304

PRIOR PLILING DATE: 2002-02-19

PRIOR FILING DATE: 1090-08-18

PRIOR PLILING DATE: 1999-08-18

PRIOR PLILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATENTIN VUMBER: US 60/159,122

NUMBER OF SEQ ID NOS: 27

SEQ ID NO 6
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Pred. No. 3.7e-78;
0; Mismatches 344;
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US-10-086-464-6
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Best Local Similarity 59.1%;
Matches 644; Conservative 0
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2106 ATTGTACAGT 2115
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us-10-086-464-1.rnpb

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Sequence 366, Application US/09938842A

Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Jeff

APPLICANT: Harper, Jeff

APPLICANT: Harper, Jeff

APPLICANT: APPLICANT: APAGENIC DENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIP1300-3

CURRENT FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 366
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10.3%; Score 201; DB 9; Best Local Similarity 58.5%; Pred. No. 1e-47;
Matches 370; Conservative 0; Mismatches 260;
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TITLE OF INVENTION: STRESS-RECOLLATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING TITLE OF INVENTION: SAME, AND METHODS OF USE CURRENT APPLICATION NUMBER: US/09/938,842A CURRENT FILING DATE: 2601-08-24 PRIOR APPLICATION NUMBER: US 60/227,866 PRIOR FILING DATE: 2000-08-24 PRIOR FILING DATE: 2000-08-24 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-01-16 PRIOR FILING DATE: 2001-06-22 NUMBER: US 60/360,111 PRIOR FILING DATE: 2001-06-22 PRIOR FILING DATE: 2001-06-20 PRIOR PRIO
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Pred. No. 7.4e-49;
0; Mismatches 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Arabidopsis thaliana US-09-938-842A-926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
10.5%;
Best Local Similarity 57.2%;
Matches 354; Conservative
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RESULT 12 US-09-938-842A-366

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CACCACAGGCATCTGGTGTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTT 1038
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                                                                                           AGCITAGITGACIGGGCACGACCATIGCTT---AACCGAGCATCIGAGCAAGGAGAC 1506
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APPLICANT: Brown, D.
APPLICANT: Zhu, T.
APPLICANT: Lan, T.
APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
TITLE OF INVENTION: Promoters for regulation of plant expression
TITLE OF INVENTION: Promoters for regulation of plant expression
TITLE OF INVENTION: 2000-06-25
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR PLING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
PRIOR FILING DATE: 2000-12-29
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Best Local Similarity 55.5%; Pred. No. 6.6e-46;
Matches 401; Conservative 0; Mismatches 312
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                Sequence 179, Application US/VS887576
Patent No. US20020144047A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ORGANISM: Arabidopsis thaliana
US-09-887-576-179
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; APPLICANT: Budworth, P.
                                                                                                                                                                                    RESULT 14
US-09-887-576-179/c
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LENGIH: 2004
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                                                                                                                          APPLICANT: Kreps, Joef
APPLICANT: Kreps, Joed
APPLICANT: ALM, TOUR
TITLE OF INVENTION: SAME, AND METHODS OF PLANTS, IRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE
FILE REFERENCE: SCRLP1300-3
CURRENT PILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2010-01-16
PRIOR FILING DATE: 2010-02-16
PRIOR FILING DATE: 2010-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         979 CACCACAGGCAICIGGIGTCTTGTTGGTTATIGCAICGCGGGGCCAAAAGAIIGCIT 1038
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Fred. No. 3.1e-47;
0; Mismatches 300; Indels
                                                                 US/09938842h
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ORGANISM: Arabidopsis thaltana
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Best Local Similarity 56.9%;
Matches 406; Conservative
                                                                 Sequence 1911, Application
Patent No. US20020160378A1
                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-938-842A-1911
                                           US-09-938-842A-1911
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1431 CAACAATGICTATGTAGATSACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGC 1490
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                        1134 IGGAICTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAATCCTAAAATCATTCACCG
                                                                                         1407 TGATGCTGCAAGAGGACTTGCATGAAGACTCGCAACCCTCCGTATACACAG
                                                                                                                                                                  1080 CCATGG-----CGAGGGACGGCCTACAATGGAATGGAGCACCAGATTGAAGATTGCTCT
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Patent No. US20020160378A1

GENERAL INFORMATION:

APPLICANT: Harper, Joef

APPLICANT: Marge, Juoel

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: Wang, Xun

APPLICANT: CANE, AND METHODS OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

TITLE OF INVENTION: SOME, AND METHODS OF USE

FILE OF INVENTION: SOME, AND METHODS OF USE

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR FILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 1079

LENGTH: 2124
                                                                            CCGGAATACGCTGCAAGCGGAAAGCTCACGGAGAAGTCTGACGTTTTCTCATTTGGCGTT 1389
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Description	BM408099 EST582426 BG596561 EST495239 BG441204 GA_EBA001 AV543493 AV543493 BM358715 GA_EBA001 AV551753 AV551753
А	BM408099 BG596561 BG441204 AV543493 BM358715 AV551753
DB	122 13 10 10 10 10 10 10 10 10 10 10 10 10 10
Length	757 757 692 584 666
& Query Match	22.7 22.1 21.3 21.2 20.6 20.6
Score	442.2 429.6 413.2 411.6 400 399
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                                                           /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: Abr]; shot; supplier: Corneal University, Tanksley lab: sequencing: The Institute for Genomic Research. Roots were isolated from in vitro grown stem cuttings on CM medium. Cuttings from in vitro grown stem cuttings on CM medium. Cuttings from in vitro grown plants on medium."
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                                                                                                                                                                  Score 442.2; DB 13; Length 759;
Fred. No. 1.6e-95;
0; Mismatches 198; Indels 0;
    /clone="cpR033021"
/clone_lib="potato roots"
/tissue_type="roots"
/dev_stage="in vitro grown stem cuttings"
/lab_host="SOLR"
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RESULT 2

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/note-"Vector: pBluescript SK(-); Site_1: BcoRI; Site_2: XhoI; Various sizes of sprouting eyes (2mm to 15mm) were taken from tubers. The tubbers were incubated at 26c in the dark for 2-3 weeks prior to sprouting. The eyes were frozen in liquid nitrogen immediately upon removal from
       EST 12-APR-2001
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757 bp mRNA linear EST 12-APR-200 CSIS Solanum tuberosum CDNA clone CSIS15A23 5' sequence,
                                                                                                                                                                     Solahum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core endicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1 (bases 1 to 757)
van der Boeven, R., Bezzerides, J., Sun, H., Cho, J., Chiemingo, A., Bougri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
Generations of Ests from sprouting potato eyes
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The Institute for Genomic Research
For clone info: please contact Research Genetics, I
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 1.7e-92;
0; Mismatches 199; Indels
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/db_xref="taxcn:4113"
/clone="cSTS15A23"
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                                               mRNA sequence.
BG596561
BG596561.1 GI:13614701
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Best Local Similarity 73.4
Matches 549; Conservative
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KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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RESULT 3 BG441204 ACCESSION

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AV543493
Av543493 Arabidopsis thaliana roots Columbia Arabidopsis thaliana cDNs av543493 arabidopsis thaliana roots Columbia Arabidopsis thaliana AV543493 arabidopsis thaliana av543493.1 GI:8714907
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Asamizu.E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
of 12,028 non-redundant expressed sequence tags from normalized and
size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                         1039 GTCTATGAGTTTGTTCCTAACAATCTCGAGCTTCACCTCCATGGCGAGGGACGGCCT 1098
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
71 GAATTAGCGAGGAACGGATGGCTTCTCGGAAGTTAACCTTCTTGGACAAGGTGGTTTT
                                                                                                                                                        GGTTACGTGCACAAAGGTGTGGTTGCCTAGTGGGAAAGAAGTTGCTGTGAAGCAGTTGAAA
                                                                                                                                                                                                  CACCACAGGCATCTGGTGTTGTTGGTTATTGCATCGCCGGTGCCAAAAGATTGCTT
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Subsyptum arboreum.

Gossyptum arboreum.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatcphyta; Magnoliophyta; eudicotyledons; core eudicots; Acsidae; eurosids II; Malvales; Malvaceae; Gossyptum.

E 1 (bases 1 to 692)

Wing R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, J., Wood, T.C., Leslie, A. and Wilkins, T.A.

An integrated analysis of the genetics, development, and evolution of the cotton fiber

L Unpublished (2000)

Contact: Wing RA

Clemson University

Colemson University

100 Jordan Hall, Clemson, SC 29634, USA

Tel: 864 656 7288

Fax: 864 656 7288
  1321 IACTTGGCTCCGGAATACGCTGCAAGCGGAAAGCTCACGAGAAGTCTGACGTTTTCTCA 1380
                                                                                      TITGESCITCICCITITGGAGCICATTACTGGACGTCGACCGTTGATGCCAACAATGTC 1440
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/clone-'6A_Ea0012C15f'
/clone_lib='Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10"
                                                                                                                                                                                                       601 GAAAASITTGATACCCTTGTTGATCGTCGGCTAGAAAAIGATTATAACCATAATGAGATG
                                                                                                                                   481 TTTGSIGTAATGCTTCTTGAGTTGATAACTGGACGTCGGCCTGTTGACTCTAATCA
                                                                                                                                                                               1441 TATGTAGATGACAGCTTAGTTGACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAA
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/organism="Gossypium arboreum"
/strain="AKA"
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Pred. No. 1.46
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1621 ATGAGCCAGATTGTGCGTGCGTTAGAAG 1648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: rwing@clemson.edu
Seg primer: TAATACGACTACTAGGG
High quality sequence stop: 690.
Location/Qualiflers
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138 c 17
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arboreum cDNA clobe GA_Ba0012D16r, mRNA sequence.
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1 (bases 1 to 666)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.
An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="RZZVIfO7F"
/clone_lib-"Arabidopsis thaliana roots Columbia"
/tissue_type="roots"
/note="Vector: pBluescriptII SK-; Site_I: EcoRI; Site_2:
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                        /organism="Arabidopsis
                                                                                                                                                                 Pred. No.
                                    /strain="Columbia"
/db_xref="taxon:3702"
Location/Qualifiers
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                                                                                                                                                                                                                                                /strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="34 Ea0012D16r"
/clone=lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              859 GGTTACGTGCACAAAGGTGTGTTGCCTAGTGGGAAAGAAGTTGCTGTGAAAGCAGTTGAAA
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                                                                                                                                                                                                                                                                                                                                                                                 /lab_host="E. coli"
/note="Yector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
134 c 167 g 187 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 666;
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Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 646
Seq primer: TAATACGACTACTATAGGG
High quality sequence stop: 666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.6%; Score 400; DB 13;
ilarity 75.6%; Pred. No. 2.1e-85;
Conservative 0; Mismatches 160;
                                                                                                                                                                                                                              /organism="Gossypium arboreum"
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HTC 25-MAY-2002
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1 (hases 1 to 1053)
1 (hases 1 to 1053)
Arthur, L.W., Hanafey, M., Morgante, M. and Tingey, S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Oppublished (2002)
2 (bases 1 to 1053)
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                                                  GGAAAGAAGTTGCTGTGAAGCAGTTGAAAGTTGGGAGTGGTCAGGGAGAGAGGGGAGTTTC
                                                                      Gaps
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/db_xref="WaizebB:637889"
/db_xref="Waoxon:4577"
/dlone="PCO134818"
/clone="PCO134818"
/clone=lib="Maize Mapping Project/DuPont Cornsensus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19.3%; Score 376; DB 11; Length 1053; 68.5%; Pred. No. 1.5e-79;
                                                                                                                                                                                                                                                                                                                    linear
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220 c 262
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Zea mays PCO134818 mRNA
AY108241
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Matches
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VERSION
KEYWORDS
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AUTHORS
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                                                                                                                                                                                                                                                                  RESULT 7
AY108241
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                                                                                                                                                                                                                                                                                                               Lease: To 573 to
                                                                      EST 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                             87551753 Arabidopsis thallana roots Columbia Arabidopsis thallana cDNA clore RZ130c07R 5', mRNA sequence.
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/tissue_type="roots"
/note="Yector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GCGGCTCCGACTACTCGGACCGTCCAGGTTCTTCCTCCACCGTCTCCAGGGCTTGIGTTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Brika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 399; DB 10;
Pred. No. 3.5e-85;
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="RZ130c07R"
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Best Local Similarity
Matches 479; Conserv
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Matches 535; Conservative
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                                                                         ACTGGGCACGACCATTGCTTAACCGAGCATCTGAGCAAGGAGCTTTGAGGTTTAGCTG 1522
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CTICTGGCAAGCIAACAGAAAAICCGAIGTATITTCCIICGGAGTCATGCIICTTGAGC 310
                                                                                      25-MAY-2002
                                                                                                                                                                                                                                                         610
                                                                                                                                                                                                                                                                                          Exaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 1016)
Halney.C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey.S.V.
Anthur,L.W., Hanafey,M., Morgante,M. and Tingey.S.V.
Overgo Probes
2 (Daylos 1 to 1016)
2 (bases 1 to 1016)
                                        ATGCAAAGATGAATAATGGGTAATGACAGAGAGGAGATGGCTCGCATGGTTGCTTGTGCTG
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                                                                                                                                                                                                                                                                                                                                                 668 AGAAGTICAAGAAGAIGGCATT-----CAACAACAATATACCAGCAGCCAATACAGCG
                                                                                                                                                                                                                                                                                                                                                                                        Anotes this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was
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Library"
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Submitted (25-APR-2002) Maize Mapping Project, University
Missouri, Columbia, MO 65211, USA
Location/Qualifiers
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/organism="Zea mays"
/db_xref="MalzebB:637888"
/db_xref="taxon:4577"
/clone="PcOl34814"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lea mays PCO134814 mRNA sequence. AXIO8243 AXIO8243.1 GI:21211321 HTC.
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EST54284 Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues Solanum tuberosum cDNA clone STMGM90 5, end, mRNA sequence.

BQ506869.2 GI:21922719
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assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" 231 c 262 g 262 t
                                                                                                                                                                                                                                                       1175 ATCCIAAAATCATTCACCGTGATATCAAGGCTTCAAACATATTGATAGATTTCAAGTTTG
                                                                                                                                                                                                                                                                          121 AAGCTAIGGTIGCTGACTIIGGACTIGGAAAGTICACTACTGATAACAACAACACCAIGTGT
                                                                                                                                                                                                                                                                                                                                                                                                                           1355 ICACGGAGAAGTCIGACGITITCICATIIGGCGIIGIGGTITIGGAGCICATIACIGGAC
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                                                                                                              DB 11; Length 1016;
                                                                                                                                                  Indels
                                                                                                              Score 366.2; DB 11;
Pred. No. 3.3e-77;
0; Mismatches 238;
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1381 TITGGCGTTGTGCTTTTGGAGCTCATTACTGGACGTCGACCGTTGATGCCAACAATGTC 1440
                                                                                                        1441 TATGTAGATGACAGCTTAGTTGACTGGGCACCACCATTGCTTAACCGAGCATCTGAGCAA
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TAG_TISSUE=roots
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Best Local Similarity 71.8°
Matches 466; Conservative
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           Entaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.

E (bases 1 to 645)

S Buell, C.R., Hart, A., Baker, B., Tanksley, S., Fry, W., Smart, C., Kararycheva, S.A.

Generation of a set of potato cDNA clones for microarray analyses Unpublished (2002)

On Jun 10, 2002 this sequence version replaced gi:21365738.

Other ESTS: EST64285

Contact: Robin Buell

The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: XhoI; supplier: Combination of untreated and Phytophthora infestans-treated libraries of stolons, leaves, leaflets, axillary buds of stem explants, petioles, germinating eyes tibes, or 154 g 192 t
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/clone_lib="Generation of a set of potato cDNA clones for microarray analyses mixed potato tissues"
/tissue_type="mixed tissues"
/lab_bost="Solk"
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Email: pointsoftgr.org
This close is available through the Research Genetics, contact the
Research Genetics for further information 1-800-711-6195 or
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                                                                                                                                                                                                                                                                                                                                                                                       1. .645
/organism="Solanum tuberosum"
/cullivar="Kennebec or Binjte"
/db_xref="taxon:4113"
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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ilarity 74.3%;
Conservative
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                                                                                         AUTHORS
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Kozik, A., Michelmore, R.W., Knapp, S., Matvienko, M., Rieseberg, L., Ini, H., van Damme, M., Lavelle, D., Chevalier, P., Ziegle, J., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Ellison, P., Kolkman, J., Slabaugh, M.S., Livingston, K., Zhou, Y., Ellison, P., Kolkman, J., and Bradford, K.

Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
Intp://compgenomics.ucdavis.edu/
Onpublished (2002)
Contact: Alexander Kozik [R.M.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Fax: 1-(530)-752-9659
Bmail: akozik@atgc.org [michelmore@vegmail.ucdavis.edu/
for Artilla kozik@atgc.org [michelmore@vegmail.ucdavis.edu/
GGBI0120.yg.abl QG_ABCDI lettuce salinas Lactuca sativa CDNA clone QGBI0120, mRNA sequence.
BQ849683.
BQ849683.1 GI:22235152
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
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/cultivar="taxon:4236"
/clone="0GB10120"
/clone="lb="0GB10120"
/lab_host="E.coli"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           construction can be obtained at http://sgpdb.ucdavis.edu/
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//organism="Sorghum bicolor"

/do_xref="taxon:4558"

/docalib="Embryo | (EM1)"

/folde="Organ: Embryos germinated for 24 hr; Vector:

pBluescript II from Lambda Zap II; Site_1: XhoI; Site_2:

ECORI: The library was made from poly-A RNA in the cloning

vector lambda ZAP II. Clones to be sequenced were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGCAGAGGTTGAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTCTCTTGTTGGTTA 1010
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, Pooldeae
, Triticeae, Triticum.
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0
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125 c 147 g 168 t
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   High quality sequence stop:
POLYA=No.
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432; Conserv
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1 (EM1) Sorghum bicolor cDNA, mRNA
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Erkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC
clade, Panicoideae, Andropogoneae, Sorghum.
                                    9
                                                                                        1117 AGATTGAAGATTGCTCTTGGATCTGCTAAAGGACTTTCTTATCTTCATGAAGATTGCAAT
                                                                                                                                                                                                                                GCTAAGGTIGCIGATTTTGGTCTTGCTAAGATTGCTTCTGATACAAACACGCATGTATCA
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                                  GAACGTGAGTTTCAGGCGGAAGTTGAGATCATTAGTCGAGTTCATCATAAACATCTCGTT
                                                                     AACAACAATCTCGAGCTTCACCTCCATGGCGAGGGACGGCCTACAATGGAATGGAGCACC
                                                                                                                                                                         121 AATAACACCATGGAATTCCACTTACATGGAAAGAATCGTCCCGTAATGGAGTTTCCCACA
                                                                                                                                                                                                                                                                                1177 CCTAAAATCAITCACCGIGATATCAAGGCTTCAAACAIATTGAIAGAITTCAAGTTTGAA
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Reid, S.P., Cordonnier-Pratt, M.-H., Gingle, A. and Pratt, L.E. B. and EST database from Sorghum: developing embryos
Unpublished (2000)
Contact: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271,
Tel: 706 542 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1537 AATGGTATGACAGAGAGAGATGGCTCGCATGGTTGCTTGTGCTGCGG 1585
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Seq primer: JEN REV
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AUTHORS
TITLE
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BF176907
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KEYWORDS
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1190

376

256

1250

96\*

SOURCE

436

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637 bp mRNA linear EST 19-APR-2002 Schmidt lab Zea mays cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .637

Organism="Rea mays"

/cultivar="OB43"
/db_xref="taxon:4577"

/clone_lib="1091 - Immature ear with common ESTs screened
y schmidtyle="Inflorescence meristem - floral organ
primordia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Organ: Immature ear; Vector: pAD-GAL4; Site_1:
ECORI; Site_2: XhoI; RNA from library 606 was filtered for
common ESTs found in 606."
                552 GGATGGTAACTATGATGAGTTAGTGGATGCTCGTCTGG3AAAGGATTTCAATCTAATGA 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   952 GCAGAGGTTGAGATCATCAGCAGAGTTCACCACAGGCATCTGGTGTTCTTGTTGGTTAT 1011
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Stanford University
Stanford University
Tel: 650 723 227
Fax: 650 725 8221
Famil: walbot(%stanford.edu
Plate: 1091014 row: D. column: 01.
                                                                     1557 GAIGGUICGCAIGGIIGCIIGIGCIECGGCIIGIG 1591
                                                                                                   0; Mismatches 163;
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/lab_host="Stratagene XLOLR"
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                                             Wheat functional genomics - Glenlea developing seeds cDNA libraries Unpublished (2002)
Contact: Dr. Sylvie Cloudier
Cereal Research Centre, Agriculture and Agri-food Canada
195 Dafoe AG Winnipeg, MB, Canada RIT 2M9
Fal: (204) 983-24604
Exi: (204) 983-4604
Email: scloutier@em.agr.ca
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/dev_stage="5 days after anthesis"
/lab_host="E. coli DH10B"
/note="Vector: pSPORT-P (Invitrogen Technologies);
NotI; Site_2: Mulu: mRNA obtained from wheat seeds cultivar Glenlea 5 days post-anthesis"
126 c 162 g 189 t
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Pred. No. 4.8e-73;
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/cultivar="Glenlea"
/db_xref="taxon:4565"
/clone="TarBC95015802R"
/clone=lib="TarBC9"
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Lettuce and Sunflower Ests from the Compositae Genome Project http://compgenomics.ucdavis.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      421 AGTTTGTTCCAAACAACACCTTGGAGTTTCACTTGCATGGGAAGGGCCGACTGACCATGG
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                                                                                                                                                                                                                                                      806 CTAGAGCCACCAATGGTTTCTCCGAGGCGAACTTGTTAGGACAAGGCGGGTTCGGTTACG
                                                                                                                                                                                                                                                                                                                                                                                                    926 GIGGICAGGGAGAGAGGGAGTIICAGGCAGAGGTIGAGAICAICAGCAGAGTICACCACA
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 Mismatches 198;
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OGG21G04, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM Gossypium arboreum
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; Core endicots:
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
E 1 (bases 1 to 679)
SW Wingy.R.A., Firsch,D., Yu.Y., Main,D., Rambo,T., Simmons,J., Henry,J., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and erolution of the cotton fiber
Of the cotton fiber
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
                                                                                                                                                                                                                                     1251
                                                                                      CTIGGATCIGCTAAAGGACTITCTIATCTICATGAAGATIGCAATCCTAAAAICATTCAC 1191
                                                                                                                                                                                                                                                                                                            TTTGGTCTTGCTAAGATTGCTTCTGATACAAACACGCATGTATCAACACGTGTGATGGGA 1311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST 22-MAY-2002
                 TGCATCGCCGGTGCCAAAAGATTGCTTGTCTATGAGTTTGTTCCTAACAACAATCTCGGAG 1071
                                    448
                                                                                                                                                                                                                                                      BQ404121 679 bp mRNA linear EST 22-MAY-200; GA_Ed0066E04f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ed0066E04f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone="GA_Ed0066E04f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                               449 TTGGGTGCTGCCAAGGGTTTAGCTTATCTTCATGAAGACTGCCATCCAAAGAICATCCAT
                                                                                                           CGTGATATCAAGGCTTCAAACATATTGATAGATTTCAAGTTTGAAGCTAAGGTTGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI*
149 c 162 g 185 t 1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
Total High Quality bases = 516
Seq primer: TAATACGACTCACTAIAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seg primer: TAATAČGACTCACTAIAGGG
High quality sequence start: 4
High quality sequence stop: 646.
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/cultivar="8400"
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Tel: 864 656 7288
Fax: 864 656 4293
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Separate CONS. were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. CDNAS were phon pooled, size-fractionated, directionally cloned finto a custom medium-copy vector and size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TNG_IIB=QG_EFGHJ lettuce serriola
TNG_IIS=QG_EFGHJ lettuce serriola
TNG_IIS=CG_EFGHJ lettuce serriola
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Fax: 1-(530)-752-9659

Fax: 1-(530)-752-9659

Fax: 1-(530)-752-9659

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pBRcDNASfiaB; The library was constructed from 10 different sources of RNA from a single genotype.
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Contact: Alexander Kozik [R.W.Michelmore]
Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
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Fred. No. 2.8e-70;
0; Mismatches 209; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="QG_EFGHJ lettuce serriola"
/lab_host="E.coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Lactuca sativa"
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Location/Qualifiers
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/db_xref="taxon:4236"
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Search completed: July 7, 2003, 10:26:51 Job time: 2874 secs

Tue Jul

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GenCore version 5.1.6
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OM protein - protein search, using sw model

2, 2003, 15:16:17; Search time 25 Seconds (without alignments) 1073.407 Million cell updates/sec July Run on:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST.....REMEMGKIKRTGQGYSGPSL 647 Title: Perfect score: Sequence:

BLCSUM62 Gapon 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length; 0 Maximum DB seq length; 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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pti	006548 arabidopsis P46573 arabidopsis P43298 arabidopsis P43298 arabidopsis 024585 zea mays (m 099929 brassica ol P47735 arabidopsis 060005 brassica ol P47735 arabidopsis 065406 mus musculu P51617 homo sapien 095652 drosophila P13983 arabidopsis 065652 drosophila P13983 arabidopsis 065652 drosophila P13498 arabidopsis 065652 drosophila P14918 zea mays (m 002817 homo sapien 00341 nicotiana t P65142 mus musculu 001411 nicotiana t P65142 mus musculu 001411 nicotiana t P34908 coturnix co P14918 zea mays (m 002817 homo sapien 064982 gallus gall 064982 gallus gall 064982 gallus gall 064982 cochliobolu 04532 cochliobolu 045316 homo sapien 04516 homo sapien
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Score	566.5 578.6 57
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Q05609 arabidopsis	PO4280 homo sapien	P07527 schizosacch	Q9j104 mus musculu	060610 homo sapien	P06599 daucus caro	P46551 caenorhabdí	P28693 gallus gall	O08808 mus musculu	P48562 saccharomyc	P23246 homo sapien	P37370 saccharomyc	
CIR1_ARATH	PRP1_HUMAN	WEE1_SCHPO	FMN2_MOUSE	DIA1_HUMAN	EXTN_DAUCA	CDK9_CAEEL	EPB2_CHICK	DIA1_MOUSE	CLA4 YEAST	SFPO HUMAN	VRP1_YEAST	
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315	312.5	311	310.5	307	306.5	300.5	300.5	297.5	297	296.5	296.5	
34	35	36	37	38	39	40	41	42	43	44	45	

## ALIGNMENTS

RESULT 1 APKA ARATH	ID APKA_ARATH STANDARD; PRT; 410 AA.	01-NOV-1995 (Rel. 32, Creat	(Rel. 32,	Protein kinase ARKIA (	GN APKIA. OS Arabidopsis thaliana (Mouse-ear cress).	Eukaryota, Viridiplantae, Streptophyta, Embryo		RP SEQUENCE FROM N.A.	 RX MEDLINE=93081726; PubMed=1450380;	hirayama 1., Oka A.; "Novel protein kinase of Arabidopsis thaliana	KL Plant Mol. Blol. 20.1535-652(1992).	SERINE/THREONINE ACTIVITY. IN VIVO, CAN PHOSPHORYLATE	RESIDUES OF LIMITED SUBSTRATES.	CC -1- SIMILARITY: BELONGS TO THE SERVTHR FAMILY OF PROTEIN KINASES.	This SWISS-PROT entry is copyright. It	between the Swiss Institute of Bioi	the European Bloinformatics Institute, Ther	modified and this statement is not removed	entities requires a license agreement (See h	CC or send an email to license@isb-sib.ch). CC	EMBL; D125	InterPro; IPR000719;	DR InterPro; IPROG4040; STY_pkinase. DR Interpro: IDROADSOA: Ser thr prinase	Pfam; PF00069; pkinase; 1	Probom;	DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.	PROSITE; PS00108; PROTEIN_KINASE_ST; 1	PROSITE; PS50011; PROTEIN_KINASE_DOM;	AW TIGHTSETSES, SETHOF/LHEOUTHE-PIOCETH KINGSE; Tyrosine-Procein Kingse; KW ATP-binding: Multigene family: Myristate.	LIPID	DOMAIN 68 352 PROTEIN	82 ATP (BY	ACT STREET 203 203 BY SIMILARITY STREET 203 203 BY STREET 203 203 BY STREET 203 203 BY STREET BY	SQ SEQUENCE 410 AA; 43319 MW; SHABZAD9EQU63U62 CKC64;	Query Match 19.0%; Score 556.5; DB 1; Length 410;	LOCAL SIMILIAILLY 39.16; FIEL. NO.

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                                                                           EKGVLP-----SGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCI
                                                                                                                               340 AGAKRILLVYEFVPNNNLELHLHGEG---RPTMEWSTRLKIALGSAKGLSYLHEDCNPKII
                                                                                                                                               143 EDEHRLIVYEFMPRGSLENHLFRRGITEÇP-LSWKLRLKVALGAANGLAFLHSS-ETRVI
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
       Gaps
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STRAIN-CV. Columbia;
MEDLINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldilyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Pail G., Van Aken S., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUNCTION: POSSIBLE BI-FUNCTION. KINASE. IN VITRO, IT EXHIBIT SERINE/IHREONINE ACTIVITY. IN VIVO, CAN PHOSPHORYLATE TYROSIN RESIDUES OF LIMITED SUBSTRATES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
    55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana,";
                                                                                                                                                                                                                                                                                                                                                       622
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  131; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
APCLEUR Kinase APKIB (EC 2.7.1.-).
APKIB OR AT3G28930 OR T914.1.
  63; Mismatches
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MEDLINE=93081726; PubMed=1450380;
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SEQUENCE OF 143-346 FROM N.A.
                          GSDYSDRPVLPPP---
 Conservative
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P46573; Q9SLH5;
01-NOV-1995 (Re.
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       a collaboration
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01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JULATIVE receptor protein kinase TMK1 precursor (EC 2.7.1.-).
TMK1 OR AT1356150 OR F15E12.4.
Arabidopsis thaliana (Mouse-ear cress).
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PROTEIN KINASE.
AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
BY SIMILARITY).
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InterPro: IPR00719; Buk_pkinase.
InterPro: IPR004040; STy_pkinase.
InterPro: IPR004040; STy_pkinase.
InterPro: IPR001245; Tyr_pkinase.
InterPro: IPR001245; Tyr_pkinase.
Pfam: PF00069; pkinase: 1.
PRINTS: PR00109; TYRKINASE.
ProDom; PD000001; Buk_pkinase; 1.
SMART; SM0221; STYRK; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE: PS00108; PROTEIN_KINASE_ATP; 1.
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PROSITE; PS50011; PROTEIN_KINASE_DOM; 1
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RELINE=21016719; PubMed=11130712;

RELINE=21016719; PubMed=11130712;

RELINE=21016719; PubMed=11130712;

RA Theologia A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Thite O., Alonso J., Altafi H., Araujo R., Eowman C.L., Brooks S.Y.,

RA Thite O., Alonso J., Chen H., Cheuk R.F., Chin C.W.,

RA Dunn P., Etgu P., Feldbluw T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Dunn P., Etgu P., Feldbluw T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Dunn P., Etgu P., Teldbluw T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Huiter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Langin-Hooper S., Lee J.M., Lorz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Lee J., Lee J.M., Lorz C.A., Li J.H., Li Y.-P.,

RA Miltscher J., Miranda M., Nguyen M., Noerman W.C., Osborne B.I.,

Radano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Rakano H., Yallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Ru J. Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Ru J. Wa Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Ru J. Yu G., Fraser C.M., Venter J.C., Davis R.W.;

Ru J. Salzberg C.M., Venter J.C., Davis R.W.;
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                            STRAIN-cv. Columbia;
MEDLINE=93076110; PubWed=1332795;
Chang C., Schaller G.E., Patterson S.E., Kwok S.F.,
Weyerowitz E.M., Bleecker A.B.;
"The TMK1 gene from Arabidopsis codes for a protein with structural and biochemical characteristics of a receptor protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: PROBABLE RECEPTOR.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: FOUND IN MOST TISSUES.
-!- PTM: AUTOPHOSPHOSITATED ON SERINE AND THREONINE RESIDUES.
-!- PTM: AUTOPHOSPHOSITATED ON SERINE AND THREONINE RESIDUES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
-!- SIMILARITY: CONTAINS 9 LEUCINE-RICH REPEATS (LRR).
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SMART; SM0370; IRR; 7.
SMART; SM00369; IRR; 7.
SMART; SM00369; IRR; 7.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
PROSITE; PS00109; PROTEIN_KINASE_DOM; 1.
Transferase; Serine-(threonine-protein kinase; ATP-binding; Transmembrane; Receptor; Glycoprotein; Signal; Repeat; Leucine-rich repeat; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR00161; LRR.
InterPro; IPR003592; LRR_out.
InterPro; IPR003591; LRR_typ.
InterPro; IPR004040; SIY_LRinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00369; pkinase; I.
Pfam; PF00360; LRR; 11.
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InterPro; IPR000719; Euk pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 408:816-820(2000)
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 SECUENCE FROM N.A
                                                                                      NCBI_TaxID=3702;
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PUTATIVE RECEPTOR PROTEIN KINASE TMK1
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                                                                                                                                                                                                                                                                                          Length 942;
           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                 104 VPGPPSNP----SREGGSPRPPSSPSPSPSDGLS---
                             CYTOPLASMIC (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                      598 QEYNATG-----EYSNPTSDYGLYPSGSSSEGQ 625
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
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                                                                                                                                                                                                                              (GLCNAC.
                                                                                                                                                                                                                                                                                                               90; Mismatches 194;
                                                                                                                                                                                                                                                                                          18.8%; Score 647.5; DB 1;
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Matches 178; Conservative
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942 AA;
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         DOMAIN
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RY STRAIN-CY. Columbia;

RY ABDLINE-21016721; DubMed-11130714;

RA Tabata S., Kareko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,

RA Tabata S., Kareko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,

RA Miyajima N., Sasamoto S., Kimura Y., Miraki A., Nakayama S.,

RA Miyazaki N., Naruoto M., Mitsuno A., Miraki A., Nakayama S.,

RA Handse M., Yasuda M., Yasuda M., Saro S., de la Bastida M.,

RA Huang E., Spiegel L., Gooj J., O'Shaughnessy A., Preston R.,

RA Huang E., Spiegel L., Gooj J., O'Shaughnessy A., Preston R.,

RA Huang E., Cordum H., Cordes M., Armstrong J., Becker M.,

RA Belter E., Cordum H., Cordes M., Armstrong J., Becker M.,

RA Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P.,

Leonard S., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C.,

RA Belter E., Cordum H., Cordes M., Hoon See L., Vil D., Baker J.,

RA Morner-McPherson C., Wollam A., Yoakur M., Bell M., Deddia N.,

RA Richoff K., Toth K., King L., Bahret A., Miller B., Marra M.,

RA Martienssen R., McCombie W.R., Milson R.K., Wurphy G., Bancroft I.,

RA Martienssen R., McCombie W.R., Milson R.K., Wurphy G., Bancroft I.,

RA Ramsperger U., Wedler H., Balke K., Weller E., Johnson S.,

Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zimmermann W.,

RA Ramsperger U., Wedler H., Balke K., Weller E., Johnson S.,

And Staveren M., Dirkse W., Mooijman P., Klein Lankhorst R.,

Reletzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S.,

RA Sequence and analysis of chromosome 5 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                        Moran T.V., Walker J.C.; "Molecular cloning of two novel protein kinase genes from Arabidopsis
                                                                                                                                                                              Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledoms; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: ROOTS, LEAVES AND STEMS. SIMILARITY: BELCHGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                 15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Probable serine/threonine-protein kinase NAK (EC 2.7.1.-).
NAK OR AT5G02293 OR TIE22_50.
                                            389 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 1216:9-14(1993).
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR002309; Ser_thr_pkinase.
Pfan; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=94032493; PubMed=8218420;
                                                                             (Rel. 32, Created)
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                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
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                                                                                                                                                                                                                                                                       NCBI_TaxID=3702;
                                                         P43293; Q9L296;
01-NOV-1995 (Re]
15-JUN-2002 (Re]
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                                       NAK_ARATH
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RESULT 4
NAK_ARATH
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ProDom; PD000001; Euk\_pkinase; 1.

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                                                                                                                                                                                                                                                                             232 FMSSSG--GSDYSDRPVLPPPSPGLVLGFSKSTFTYEELARAINGFSEANLLGQGGFGYV 289
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                                                                                                                                                                                                                                                   19; Gaps
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SUBCELLAR LOCATION: Type I membrane protein.

SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

SIMILARITY: CONTAINS I THER-CYS REPEAT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. B73;
MEDLINE=96355669; PubMed=8703079;
Becraft P.W., Stinard P.S., McCarty D.R.;
"CRINKLIft: A INFR-like receptor kinase involved in maize epidermal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Putative receptor protein kinase CRINKLY4 precursor (EC 2.7.1.-).
                                                                                                                                                                                                                   Length 389;
SWART; SW00221; STYKC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding.
DOMAIN 68 353 PROTEIN KINASE.
NP_BIND 74 82 ATP (BY SIMILARITY).
106 ATP (BY SIMILARITY).
                                                                                                                                                BY SIMILARITY.
G -> V (IN REF. 1).
58Alla78515898E3 CRC64;
                                                                                                                                                                                                                 18.1%; Score 626.5; DB 1; 41.1%; Pred. No. 1.7e-17;
                                                                                                                                                                                                                                                64; Mismatches 113;
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                                                                                                                                                                                                                                                Matches 137; Conservative
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106
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389 AA;
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Science 273:1405
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or send an email to license@isb-sib.ch).
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82; Mismatches 129; Indels
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52F8481AC187E061 CRC64;
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AIP (BY SIMILARITY).
AIP (BY SIMILARITY).
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PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00050; TNRR_NGFR_1; FALSE_NEG
PROSITE; PS50050; TNRR_NGFR_2; 1.
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                                                                                                           InterPro; IPR000719; Euk_pkinase.
InterPro; IPR004040; STY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                     ProDom: PD000001; Euk_pkinase; 1.
SWART; SW00221; STYKC; 1.
SWART; SW00208; TNFR; 1.
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Pfam; PF00069; pkinase;
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RP SEQUENCE FROM N.A.

STRAIN-CY. Columbia;

RA FINELINE-21016719; PubMed-11130712;

RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Theologis A., Can L., Conway A.B., Conway A.R., Chin C.W.,

RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.B., Cheasy T.B.,

ROUND P., Etqu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Ensen N.F., Hughes B., Huizar L.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin B.,

RA C.J., K.C. H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Langin-Hooper S., Lie A., Lucos J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Lucos J.S., Maiti R., Marziali A.,

Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Bal G., Peterson J., Phan P.K., Rizzo M., Ronoey T., Rowley D.,

RA Sakano B., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome I of the plant Arabidopsis

"T. Sequence and enalysis of chromosome I of the plant Arabidopsis
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                                                                                                                                                              CIVI_ARATH STANDARD; PRI: 980 AA.

GSSTQB: 0043480; QSTGT2;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-CT-2001 (Rel. 40, Last sequence update)
16-CT-2001 (Rel. 41, Last annotation update)
Receptor protein kinase CLAVATA1 precursor (EC 2.7.1.-).
CIVI OR AR1675820 OR T40.12.
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Erassicales; Brassicaceae; Arabidopsis.
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-i- SUBGRILULAR LOCATION: Type I membrane protein (Potential).
-i- SISSUE SPECIFICITY: IN A CENTRAL REGION OF THE SHOOT AND IN BARLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark S.E., Williams R.W., Meyerowitz E.M.;
"The CLAVATA gene encodes a putative receptor kinase that controls shoot and floral meristem size in Arabidopsis.";
[Cell 89:575-585(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Williams R.W., Clark S.E., Meyerowitz E.M.;
Genetic and physical characterization of a region of Arabidopsis
chromosome 1 containing the CLAVATA1 gene.";
Plant Mol. Biol. 39:171-176(1999).

    -i- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
    -i- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).

                              608 NPTSDYGLYPSGSSSEGQTTREMEMGKIKR 637
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MEDLINE=99178804; PubMed=10080719;
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MEDLINE=97304386; PubMed=9160749;
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Nature 408:816-820(2000).
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139; Conservative
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PRODOJ; ILDRICHRSE.
PROSITE; PRODOJ; ILR. 18.
PROSITE; PSOULO7; PROTEIN_KINASE_ATF; FALSE_NEG.
PROSITE; PSOULO8; PROTEIN_KINASE_DOM; 1.
Receptor; Differentiation; Signal; Repeat; Lewcine-rich repeat; Transferase; Serine-function; Signal; Repeat; Lewcine-rich repeat; Phosphorylation; Transmembrane.
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EMBL, AC007356; AARZ6772.1; AII_INIT.
ILITEPPO; IPR000719; ENL_PKinase.
InterPro; IPR001611; LRR.
                                                                                                                                                 InterPro; IPR003592; LRR_out.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfan; PF00069; pkinase; 1.
Pfan; PF00560; iRR; 18.
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SO PRESENTATION OF THE PROPERTY OF THE PROPERT
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Length 980;

579.5; DB 1; No. 2.2e-15;

Score :

16.88; 34.88;

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11;
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STRAIN=CV. 8685; IISSUB=Stigma;

MEDLINE=92020942; PubMed=1681543;

MEDLINE=92020942; PubMed=1681543;

A fatin J.C., Howlett B., Boyes D.C., Nasrallah M.E.;

The self-incompatibility locus of Brasslea oleracea.";

The self-incompatibility locus of Brasslea oleracea.";

The proc. Natl. Acad. Sci. U.S.A. 8818816-8820(1991).

THE PROC. NATL. Acad. Sci. U.S.A. 8818816-8820(1991).

THE PROC. NATL. ACAD. IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM

THE SELLIANTION; PROBABLY ACTING IN COMBINATION WITH A LIGAND IN THE

EXTRACELLULAR DOMAIN.

CYTOPLASMIC DOMAIN.

THE REPRESENT ATP A PROCEDIN RINASE ACTIVITY OF THE

CYTOPLASMIC DOMAIN.

THE STREED PROCEDIN. IN THE PISTIL AND ANTHER.

TISSUE SPECIFICITY: PREDOMINANTY IN THE PISTIL.

THE EXTRACELLULAR DOMAIN.

S. C. I. POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN

B. CLERACEA. POSSIBLY PROVIDING THE RECONITION SPECIFICITY.

THE STRAINTY: THE EXTRACELLULAR DOMAIN IS

SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
                                                                                     187 PYGGOOOQWROONATPPSDHVVTSLPPPPKAPSPPROPPPPPPPPFMSSSGGSDYSDRPV 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --SDHNHTAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 KIIHRDIKASNILIDFKFEAKVADFGLAKIASD-INTHVSTRVMGTFGYLAPEYAASGKL
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1995 (Rel. 32, Last annotation update)
Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
61;
65; Mismatches 134; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KMNNGYDREEMARMVACAAACVRHSARRRPRMSQIVRAL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   593 PLGG---QFLVFNETSFAGWTYLCLPHRVSCPTRPGQT-
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                                                                                                                                                                                                                                                                 ---PGLVI--
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/armounce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   674 MARIFERDETEANTMKVVGTYGYMSPEYAMYGIFSEKSDVFSFGVIVLEIVSGKKNRGFY 733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           734 NLDYENDLLSYVWSRWKEGRALEIVD-PVIVDSLSSQPSIPQPQEVLKCIQIGLLCVQEL 792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 VLGFSKSTFT----YEEL-----ARAINGFSEANLLGQGGFGTVHKGVLPSGKEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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H SIMILARITY.

N-LINKED (GLCNAC. .) (POTENTIAL).

N-TINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                                                                                          PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
ITAIDSferase; Scrine/threonine-protein kinase; Signal; ATP-binding; Iransmembrane; Receptor; Glycoprotein; Self-incompatibility.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
                                                                                                                                                                                                                                                                                                                                                     PUTATIVE SERINE/IHREONINE KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.6%; Score 572; DB 1; Length 849; 32.3%; Pred. No. 3.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL. CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                         PROTEIN KINAŠE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83; Mismatches 119;
                           or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                             InterPro; IPR004040; SIY_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR000858; Slocus_glycop.
                                                                                                                                                                                                                                                                                                                                                                     RECEPTOR
                                                      EMBL; M76647; AAA33000.1; ALT_TERM
                                                                   IPR001480; B_lectin.
IPR000719; Euk_pkinase.
IPR003609; Pan_app.
                                                                                                                                                                      Pfam; PF00954; S_locus_glycop; 1.
Pfam; PF01453; Agglutinin; 1.
ProDom; PD000001; Euk_pkinase; 1.
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                                                                                                                                                                                                                  SMART; SM00108; 3_lectin; 1.
SMART; SM00473; PAN_AP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                     Pfam; PF00069; pkinase;
                                                                                                                                                                                                                                                 SM00221; STYKC;
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442 4
849 AA;
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447
467
528
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Best Local Simil
Matches 139; (
                                                                                     InterPro;
                                                                                                 InterPro;
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TRANSMEM
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CARBOHYD
CARBOHYD
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CARBOHYD
CARBOHYD
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DOMAIN
NP_BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                      SIGNAL
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RAY SEQUENCE READ NATA.

RAY STRIATECT. COlumbia.

RAY STRIATECT. COlumbia.

RAY MEDITAL 20083488 PubMed-10617198;

RAY MEDITAL 20083488 PubMed-10617198;

RAY MEDITAL 20083488 PubMed-10617198;

RAY RELAY Schmeller C., Wanbutt R., Dermaler B., Mache R., Muteller M., Ray Heichselgartner K., of Sincher W., Schmidthadia T., Ray Ratin M., Delay M., Pulgdomenech P., Ratson W., Schmidthadia T., Raichert B., Portecelb D., Perez-Alonso W., Bourty M., Bancroft I., Raichert B., Portecelb D., Perez-Alonso W., Bourty M., Bancroft I., Radohan S.-A., McCullagh B., Bilham I., Robben J., Robben J., Bancroft I., Raw Raken M., Wellfels J., Almerman R., Wedler J., Vooben J., Robben J., Robben J., Robben J., Raken M., Selber B., Bancroft I., Pereken M., Dirkse W., Banchert B., Wan den Daele H., Braken M., Wellfels J., Voot M., Bastisens I., Aert R., Defoor B., Ray Mooijman P., Rein Lankhorst R., Voot M., Lamberth S., Van den Daele H., Bernels S., Fachpausch M., Lamberth S., Van den Daele H., De Reyser A., Buysshart C., Gielen J., Villarroel R., Dercer B., Braken M., Banckort B., Voot M., Bancroft S., Van den Daele H., De Reyser A., Buysshart C., Gielen J., Villarroel R., Dercer B., Braken M., Rogers J., Cronin A., Owall M., Eray M., Leohner D., Herzl R., Borkova D., Bloccker H., Schrafe M., Calmen V., Rechman S., Ray M., Lennard N., McLay K., Parken S., Gabel C., Fuchs M., Partann B., Granderath K., Dauner D., Herzl A., Rahman S., Argiriou A., Vittale D., Lignori R., Parken M., Schmidt W., Lecharny A., Aubourg S., Ginbal S., Hiller R., Schmidt W., Lecharny A., Aubourg S., Rahman D., Haase D., Lignori R., Parken M., Schmidt S., Ray M., Lennard D., Rardes D., Hanson D., Rasen D., Mancia E., Schmidt W., Lecharny A., Schwel S., Schmidt W., Berthell D., Couther R., Parken M., Schwig S., Parken J., Parken M., Willer R., Schwig S., S
                                                                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              *Receptor-like protein kinase genes of Arabidopsis thaliana."; Plant J. 3:451-456(1993).
                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequence update)
15-70N-2002 (Rel. 41, Last annotation update)
Receptor-like protein kinase 5 precursor (EC 2.7.1.-).
RLK5 OR AT4G28490 OR F2109.180.
                                                                                                                                           999 AA.
                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Columbia;
MEDLINE=94035150; PubMed=8220453;
                                                                                                                                                                                   (Rel. 33, Created)
535 ARREPRINSOIV 545
                                     793 AEHRPAMSSVV 803
                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3702;
                                                                                                                                                                               01-FEB-1996
                                                                                                                                         RLK5_ARATH
P47735;
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Bukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
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                                                                                          109095
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"Cloning of mouse IRAK.";
                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
     210
269
282
452
452
576
697
7111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                          999 AA;
                                                                                                                     Best_Local Similarity
Matches 128; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                              7117
819
7117
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                                                                                                                                                                                                                                                                                                                                                                                                               IRA1_MOUSE
062406;
                       CARBOHYD
                                                                      ACT_SITE
MUTAGEN
                                                                                                                                                                                      316
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     CARBOHYD
                CARBOHYD
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                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseelisb-sib.ch).
                                                                          "Biochemical properties of the autophosphorylation of RLK5, a receptor-like protein kinase from Arabidopsis thaliana.",
Blochim, Biophys. Acta 1208:65-74 (1994).
-1- CCFACTOR: HAVE SIGNIFICANTLY GREATER ACTIVITY IN THE PRESENCE OF MA2+ THAN MG2+.
-1- IISSUE SPECIFICITY: EXPRESSED IN ROOTS AND ROSETTES.
-1- PTM: AUTOPHOSPHORILATED ON SERINE AND THREONINE RESIDUES.
-1- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                        Leucine-rich repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
then E., Marra M., Marttenssen R., McCombie W.R.;
Sequence and analysis of chromosome 4 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RECEPTOR-LIKE PROTEIN KINASE 5.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                         Transferase; Serine/threonine-protekn kinase; ATP-binding;
Transmembrane; Glycoprotein; Phosphorylation; Leucine-rich
Repeat; Signal 14 POTENTIAL.
                                                                                                                                                             -!- SIMILARITY: CONTAINS 18 LEUCINE-RICH REPEATS (LRR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRR 18.
PROTEIN KINASE.
                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00107; PROTEIN KINASE A.P; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                   EMES, ALO21749; CAA16889-1, --
EMES, ALO21749; CAA16889-1, --
EMES, ALO2172; CAB79651.1; --
ILLEPPRO: IPR00019; ENL_PKinase.
INTERPRO: IPR001611; LRR.
INTERPRO: IPR003592; LRR_out.
INTERPRO: IPR003592; LRR_out.
Ffam; PF00069; pkinase; 1.
Pfam; PF00069; pkinase; 1.
Pfam; PF00060; LRR; 20.
PRIPMS, PRO00001; ENL_PKINASE;
PRODOM: PD000001; ENL_PKINASE; 1.
SMART; SM00370; LRR; 17.
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                                              CHARACTERIZATION.
MEDLINE=94368830; PubMed=8086440;
Horn M.A., Walker J.C.;
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                           Mature 402:769-777(1999)
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CARBOHYD
                    thaliana
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423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     726 SDSLNRDVFAAEVETLGTIRHKSIVRLWCCSSGDCKLLVFEYMFNGSLADVLHGDRKGG 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       483 DDSLVDWARPLINRASEQGDFEGLADARMNNGYDREEMARMVACAAACVRHSARRRPRMS 542
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            424 -ASDINTHVSTRVMGIFGYLAPEYAASGKLIEKSDVFSFGVVLLELITGRRPVDANNVYV
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"Developmental and tissue-specific expression of mouse pelle-like
protein kinase. 27:117609-17612(1996).
J. Biol. Chem. 27:117609-17612(1996).
-!- FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KINASE ASSOCIATES WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata, Vertebrata, Buteleostomi,
Sciurognathi, Muridae, Murinae, Hus.
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                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-CCT-2001 (Rel. 40, Created)
16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
11c-CCT-2001 (Rel. 40, Last annotation update)
11ct-cleukin-1 receptor-associated kinase 1 (EC 2.7.1.-) (IRAK-1)
17aKK) (Pelle-like protein kinase) (mPLK).
                                                                                                                                                                                                                                                                                                                            38;
(POTENTIAL)
                                                                         (POTENTIAL)
                                                                                                                                                                                                K->E: LOSS GF CATALYTIC ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  543 QIVRALE --- GNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDM 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       559 KVVIMIQEVSGAVPCSSPNTSKR-----SKTGGKL---SPYYTEDL 996
                                                                                                                                                                                                                                                                             Length 999;
                                                                                                                                                                                                                                                                                                                          61; Mismatches 121; Indels
                                                                                                                                                                                                                        MW; F5793D899EA0C6A7 CRC64;
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ATP (BY SIMILARITY).
BY SIMILARITY).
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MEDLINE=96279287; PubMed=8663605;
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InterPro; IPR000719;
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                                                                                                                         487 PQLGLA-
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           476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE IL-1 RECEPTOR IL1-R-1. THIS ASSOCIATION IS RAPID AND IL-1
DEPENDENT (BY SIMILARITY).
TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, FOLLOWED BY KIDNEY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252 PGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSG-
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                                                                         DEVELOPMENTAL STAGE: EXPRESSED FROM E11 DAY TO E18 DAY.
PTM: AUTOPHOSPHORYLATED. AN EXTENSIVE PHOSPHORYLATION OF IRAK
OCCURS AFTER ITS ASSOCIATION WITH ILL-R-1. THIS STEP COULD BE
LINKED TO THE ACTIVATION OF THE KINASE (3Y SIMILARITY).
SIMILARITY: SELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels 209;
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R WELL AFIO3876; ABD1224.1; ALT_INIT.

R InterPro; IPR002488; Death.

R InterPro; IPR00299; Buk pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R InterPro; IPR001245; Tyr_pkinase.

R Pfam; PF00653; Geath; 1.

R PR0511; Geath; 1.

R PR0511E; PS00010; Buk_pkinase; 1.

R SMART; SW00219; TyrKc; 1.

R SMART; SW0019; PROTEIN KINASE_AIP; 1.

R PR0511E; PS00101; PROTEIN KINASE_DOM; 1.

R PR0511E; PS00101; PR0TEIN KINASE_DOM; 1.

R PR0511E; PS00101; PR0FINITIN KINASE_DOM; 1.

R PR0511E; PS00101E; PR0FINITIN KINASE_DOM; 1.

R PR0511E; PS0010E; PR0FINITIN KINASE_DOM; 1.

R PR0511E; PS0010E; PR0FINITIN KINASE_DOM; 1.
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Best Local Similarity 26.7%
Matches 174; Conservative
                                                         AND SKELETAL MUSCLE.
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SEQUENCE
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                                                                                                                                                                        427 OGAKTKYLKDLIEDEAEEAGYTLKSTOPTLWWGVATDAWAAPIAAQIYKKHLDSRPGPCP 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
          WARPLENRA-----SEQGDFE 504
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Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
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MEDLINE=90294911; PubMed=2163028;
Walker J.C., Lhang R.;
"Relationship of a putative receptor protein kinase from maize to the S-locus glycoproteins of Brassica.";
Nature 345:743-746(1990).
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STRAIN=CV. B73;
Shaug R., Walker J.C.;
Submitted (OCT-1992) to the EMBL/GenBank/DDBJ databases.
-1- FUNCTION: PROBABLE RECEPTOR. INTERACTION WITH A LIGAND IN THE EXTRACELLULAR DOMAIN IRIGGERS THE PROTEIN KINASE ACTIVITY OF THE CATOPALASING DOMAIN.
-1- CATALITIC ACTIVITY: AIP + a protein = ADP + a phosphoprotein.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- TISSUE SPECIFICITY: EXRRESSED PREDOMINARLY IN THE SHOOTS AND ROOTS OF YOUNG MAIZE SEEDLINGS, AND TO A LESSER EXIENT IN THE
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SINITARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
A SER/THR-PROTEIN KINASE CLOSELY RELATED TO RAF KINASES.
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Putative receptor protein Kinase ZMPK1 precursor (EC 2.7.1.37).
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FWRT: X67733: CAA47962.1; -.
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-DANNYYVDDSLVD-
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Ser\_thr\_pkinase.

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PELLE SUBFAMILY.
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239 . 2
338 . 3
196 . 1
532 . 5
                                         SEQUENCE FROM N.A.
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Best Local
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                                                                                                                                                    PUTATIVE RECEPTOR PROTEIN KINASE ZMPK1.
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01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2501 (Rel. 40, Last annotation update)
Interlexin-1 receptor-associated kinase 1 (BC 2.7.1.-) (IRAK-1).
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Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                   R PROSITE; PSOU107; PROTEIN KINASE AIP; 1.

R PROSITE; PSOU108; PROTEIN KINASE_SI; 1.

R PROSITE; PSOU101; PROTEIN KINASE_SI; 1.

W Transferase; Serine/threonine-protein; Signal.

I Transfermbrane; Receptor; Glycoprotein; Signal.

I CHAIN 29 817 PUTATIVE RECEPTOR PROTEIN KINASE

I CHAIN 29 817 PUTATIVE RECEPTOR PROTEIN KINASE

I DOMAIN 473 498 POTENTIAL.

I DOMAIN 473 498 RT CYTOPLASKIC (POTENTIAL).

I DOMAIN 454 817 CYTOPLASKIC (POTENTIAL).

I DOMAIN 454 817 ROTEIN KINASE

I NP_BIND 540 548 ATP (BY SIMILARITY).

R SIMILARITY).
                                                                                                                                                                                                                                                                                                                         14.8%; Score 512.5; DB 1; Length 817;
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Live 52; Mismatches 111; Indels
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      Ffan, PF00024; PAN; 1.
Ffan, PF00069; pkinase: 1.
Ffan, PF005054; S_locus_glycop; 1.
Ffan, PF01453; Agglutinin; 1.
ProDom: PD000001; Euk_pkinase; 1.
SWART; SW00103; Blecin; 1.
SWART; SW00181; EGF; 1.
IPROCO858; Slocus_glycop.
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4atches 118; Conser'
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562
658
128
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P51617;
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CARBOHYD
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83 LVHILTHLQLL----RARDIITAWHPPAPLPSPGTTAPRPSSIPAPAEARAWSPRKLPSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----ATPPSDHVVISLPPPPKAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPSP
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74; Mismatches 211; Indels 134; Gaps
                                                                                                                                                                                                                                                                                         Reichwald K., Kioschis P., Rosenthal A., Platzer M.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: INVOLVED IN IL-1 PATHWAY. THIS KINASE ASSOCIATES WI
THE IL-1 RECEPTOR IL1-R-1. THIS ASSOCIATION IS RAPID AND IL-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- TISSUE SPECIFICITY: SEEMS TO BE UBIQUITOUS, ALTHOUGH PRESENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACTIVATION OF THE KINASE. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
Cao Z., Henzel W.J., Gao X.;
*IRAK: a kinase associated with the interleuxin-1 receptor.";
Science 271:1128-1131(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- PTM: AN EXTENSIVE PHOSPHORXLATION OF IRAK OCCURS AFTER ASSOCIATION WITH ILL-R-1. THIS STEP COULD BE LINKED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR00048E; Death.
InterPro; IPR000715; Buk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR002590; Ser_thr_pkinase.
Fram; Pr00069; pkinase; 1.
Fr00m; Pr00531; death; 1.
Fr00m; PS001001; Buk_pkinase; 1.
Fr00m; PS00107; PROFINI, RINASE_ATP; 1.
FR0SITE; PS00108; PROFINI, RINASE_ATP; 1.
FR0SITE; PS00111; PROTEIN_KINASE_DOM; 1.
Iransferase; Serine/threonine-protein kinase; ATP-binding.
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                                                                                                                                                               Platzer M., Bauer D., Drescher B.;
Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F -> S (IN REF. 1).
S -> L (IN REF. 1).
A7ADED75D3A3981D CRC64;
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ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF030876; AAC08756.1; -. EMBL; AF031075; AAF21636.1; -.
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239
338
196
532
5532 S
76536 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genew; HGNC:6112; TRAKI.
MIM; 300283; -.
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                                             RFAGSSPSQSSWVARTQTVRGTLAYLPEEXIKTGRLAVDIDTFSFGVVVLETLAGQRAVK 425
         RPIMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKI- 423
                                                                                                                                                                                                                                                                                                             THGARTKYLKD-LVE-----EEAEEAGVALRSTQSTLQAGLAADAWAAPIAMQIYKKHL 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --DYDSSQYNEDMKKFRKMALGIQEYNAT 603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         535 ASCIPPSPQENSIVSSTGRAHSGAAPWQPLAAPSGASAQAAEQIQRGPNQPVESDE--SL 592
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                                                                                                                                                                                                                                                                                                                                                                          ----CAAACVRHSARRPRMSQIVRALEGNVSLSDLNEGMRPGQSNV
                                                                                                                                   ----ASDINTHVSTR---VMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPV-
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MEDLINE=91017504; PubMed=1699225;
Adair W.S., Apt K.E.;
"Cell wall segeneration in Chlamydomonas: accumulation of mRNAs encoding cell wall hydroxyproline-rich glycoproteins.";
Proc. Natl. Acad. Sci. U.S.A. 87:7355-7359(1990).
-: FUNCTION: Major component of the outer cell wall W6 (crystalline)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Glycosylated polyproline II rods-with-kinks as a structural motif plant hydroxyproline-rich glycoproteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEYSNPTSDYGLYPS------GSSSEGQTTREMEMGKIKRTGQGYSGP 645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGLSAALRSWHLTPSCPLDPAPLREAGCPQGDTAGESSWG-----SGP 635
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SEQUENCE FROM N.A.
MEDLINE=21159092; PubMed=11258910;
Ferris P.J., Woessner J.P., Waffenschmidt S., Kilz S., Drees J.,
Goodenough U.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9FPQ6; Q03927;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Vegetative cell wall protein gpl precursor (Hydroxyproline-rich
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-!- PTM: N-glycosylated and O-glycosylated.
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EMBL; M58496; AAA69706.1; ALT_SEQ.
GlycoSuiteDB; Q9FPQ6; --.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydomonas reinhardtii.
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                                                                                                                                                                                   366
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InterPro; IPR002965; F\_rich\_extensn.
InterPro; IPR003882; Pistil\_extensin.

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                                                                                                                                                                                                                                                                                             ----PPSPPTPSTPGSPPPL----POPSPPAPTTPGSP----PAP--VTPPTRNPP-
                                                                                                                                                                                                                                                                                                            155 LICLLCKKKRRRDEEDAYYVPPPPPPPPPRAGGFYGGQQQQWRQQNATPPSDHVVTSLPPP
                                                                                                                                                                                                                                   5 PSPGTGS--PPSPPSNSTTTTPPPASAPPPTTPSSPPPPSTIPTSPPPSSRSTPSAP---
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. Columbia; IISSUB-Green siliques;
MEDLINE-9403320; PubMed-8219075;
Valon C., Smalle J., Goodman H.M., Giraudat J.;
"Characterization of an Arabidopsis thaliana gene (IMKL1) encoding a putative transmembrane protein with an unusual Kinasc-like domain.";
Plant Mol. Biol. 23:415-421(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia; MEDLINE-20363099; PubHed=10907853; Raneko T., Katoh T., Sato S., Nakamura A., Asamizu E., Tabata S.; Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the 4.251,695 bp regions covered by 90 Pl, TAC and BAC clones.";
                                                                       49 X 5 AA APPROXIMATE PESFX REPEATS.
POLY-PRO.
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
N-LINKED (GLCNAC. . . ) (POTENTIAL).
                                                                                                                                                                                                            78;
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-!- SUBCELLUIAR LOCATION: Type I membrane protein.
-!- SIMILARITY: TO PROTEIN KINASES IN THE C-TERMINUS. BUT DOES SEEM TO HAVE CONSERVED A KINASE ACTIVITY.
-!- SIMILARITY: CONTAINS 7 LEUCINE-RICH REPEATS (LRR).
                                             POTENTIAL.
VEGETATIVE CELL WALL PROTEIN GP1
                                                                                                                                                                               Length 555;
                                                                                                                                                 6A584A90465502F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     215 PKAPSPPRQP-PPPPPPFMSSSGGSDYSDRPVLPPPSP 252
                                                                                                                                                                                                                                                                                                                                                                                297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83;
                                                                                                                                                                           12.6%; Score 434; DB 1; 36.9%; Pred. No. 3.4e-10;
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                                                      555
339
279
279
839
N-1
495
N-1
54219 MW;
PR01217; PRICHEXTENSN. PR01218; PSTLEXTENSIN.
                                Signal.
                                                                                                                                                                                        Local Similarion
des 103; Conservative
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                             Glycoprotein; Repeat; SIGNAL 1 23
                                                                                                                 455
493.
555 AA;
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                                                                                                                              CARBOHYD
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PRINTS;
               PRINTS;
                                                                       DOMAIN
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 SREGGSPRPPSSPSPSPSPSDGLSTGVVVGIALGGVALLVIVT--LICLLCKKKRRR--- 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFEGNSPSICGLPLKPCLGSSRLSPGAVAGLVIGLMSGAVVVASLLIGYLQNKKRKSSIE 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 NLLGQGGFGYVHKGYLPSGKEVAVKQLKVGSGQGEREFQAEVELISRVHHRHLVSL-VGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   338 CIAGAKRLLVYEFVPNNNLE--LHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   396 IHRDIKASNILIDFKFEAKVADFGLAKIASDINTHVSTRVMGTFGYLAFEYAASGKLTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 116; Gaps
                                                                                                                                                                                                                             PROTEIN_KINASE_DOM; 1.
nbrane; Glycoprotein; Signal; Leucine-rich repeat;
                                                                                                                                                                                                                                                                             PUTATIVE KINASE-LIKE PROTEIN TMKL1.
EXTRACELLULAR (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 674;
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                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
PROTEIN KINASE LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65; Mismatches 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%; Score 374;
26.8%; Pred. No. 6
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                                                                                            EMBL; X72863; CAA51385.1; -.
EMBL; AP000740; BAB01215.1; -.
PIR, S35397; S35397.
PIR, S39476; S39476.
InterPro; IPR0050719; Euk_pkinase.
InterPro; IPR0050719; Euk_pkinase.
PiterPro; IPR0050519; Euk_pkinase.
PiterPro; IPR005059; LRR_out.
PiterPro; PF00069; pkinase; 1.
Piterpro; PF00069; LRR; 5.
                                                                                                                                                                                                                                                                                                                                                                          45.07
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                                                                                                                                                                                                                                        Receptor; Transmembrane;
                                                                                                                                                                                                                SMARI; SM00370; LRR; 4
PROSIZE; PS50011; PROTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183
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Best Local Similarity
Matches 129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  674 AA;
                                                                                                                                                                                                       PD0000CG
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90
95
110
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226
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CARBOHYD
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                                                                                                                                                                                                       Probom;
                                                                                                                                                                                                                                                       Repeat.
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REPEAT
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RA Adams M.D., Celniker S.E. Li P.W., Evans C.A., Gocayne J.D., Adams M.D., Celniker S.E. Li P.W., Hoskins R.A., Galle R.F., Surfice P.G., Scherer S.E. Li P.W., Hoskins R.A., Galle R.F., Sutton G.G., Wortan J.R., Yandell M.D., Zhang Q., Chen L.X., Sutton G.G., Wortan J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Bazter E.G., Fell G., Chenner M., Hedefreson S.N., RA Brandon R.C., Bazter E.G., Fell G., Nelson C.R., Millos G.L.G., Rand R. M., Basu A., Baxnedlale J., Baztatkaroglu L., Beasley B.M., Ball W.M., Basu A., Baxnedlale J., Baztatkaroglu L., Beasley B.M., Belson K.Y., Benos P.W., Berman B.P., Bhandari D., Bolshakov S., Bhille C., Bucker D., Botchan M.R., Buck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Changra R.A. Borkova D., Delcher A., Deng Z., May S.D., Dew J., Dietz S.M., Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Planser K., Doup L.E., Downe M., Dugan-Rocha S., Dlunkov B.C., Dunn P., Burlis K.J., Evangelista C.C., Ferraz C., Ferriera S., Planser K., Gloden K.J., Evangelista C.C., Ferraz C., Ferriera S., Planser K., Gloden K.J., Bowland T.J., Hernandez J.R., Houck J., Houk J., Murbin B.B., Karpin D., Lai Z., Liang Y., Lin X., Mattel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Liang Y., Lin X., Mattel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Moshel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Moshel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Moshel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai S., Moshel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Moshel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Rese M., Murphy B., Warphy B., 
                                                                                                                   616 PMEEG-----LVHALKLAMGCCAPVTTVRPSMEEVVKQLEEN-----RPRNRSAL
                     511 -MINGIDREEMARMYACAAACVRHSARRPRMSQIVRALEGNVSLSDLNEGMRP-GQSNV
SDVFSFGVVLLELITGRRPVDA---NNVYVD-DSLVDWARPLLNRASEQGDFEGLADAK-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shelton C.A., Wasserman S.A.; Pelle aroodes a protein Kinase required to establish dorsoventral polarity in the Drosophila embryo."; Cell 72:515-525(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLL OR CG5974.
Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Bexapoc Insecta; Pterygota; Meroptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                           005622, 09VB57, 001 Rd. 30, Created) 01-0CT-1994 (Rel. 30, Created) 01-0CT-1994 (Rel. 30, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Probable serine/threonine-protein kinase pelle (EC 2.7.1.37). PLL OR CG5974.
                                                                                                                                                                                                                                                                                                                                               501 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AND MUTAGENESIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-20195006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND MUTAGENESI
MEDLINE=93177834; PubMed=8440018;
                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                570
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 PPSDHVVTSLPPPFKAPSPPRQPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKS 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 T-----FIYEELARAINGFSEANLLGQGGFGYYHKGYLPSGKEYAVKQLKVGS-- 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 -GQGEREFQA---EVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLAGEGR 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                249 IDQKAYELQQSYNELKYLNSIRHDNILALYGYSIKGGRPCLVYQLAKGGSLEARLRAHKA 308
                                                  CRYSTALLOGRAPHY (2.00 ANGSTROMS) OF 26-129 IN COMPLEX WITH TUBE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRSVPTISELRAAPDSSAKVNNGPPPPSSSGVSNSNNNRTSTTATEEIPSLESLGNIHIS
                                                                                                                            -!- FUNCTION: REQUIRED FOR THE NUCLEAR IMPORT OF THE DORSAL PROTEIN WHICH ESTRELISHES DORSOVENTRAL POLARITY IN DROSOPHILA EMBRYOS.
-!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-!- SUBUNIT: Interacts with Tube through their respective N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   190 TVQRAAESLLEIDTAELENATDGWSPDNRLGQGGFGDVYRGKWKQ-1LVYAIKVMNYRSPN
                                                             **MEDILINE=20055599; PUBMed=10589683; Xiao T., Towb P., Wasserman S.A., Sprang S.R.; "Inter-dimensional structure of a complex between the death domains cell 99:545-555(1999).
                                                                                                                                                                                          -!- DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT THE LIFE CYCLE WITH HIGHEST LEVELS IN 0-3 HOUR-OLD EMBRYOS AND ADULT FEMALES.
-!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 367.5; DB 1; Length 501; Pred. No. 9.4e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4B29E2B40ACB81A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K->R: ABOLISHES ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D->A: REDUCED ACTIVITY.
A->E: REDUCED ACTIVITY.
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEATH.
PROTEIN KINASE.
ATP (BY SIMILAR:
ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57; Mismatches
                                                                                                                                                                                                                                  PELLE SUBFAMILY.
SIMILARITY: CONTAINS 1 DEATH DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS00108; PROTEIN KINASE ST: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00108; PROTEIN KINASE ST: 1.
PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS50017; DEATH_DOMAIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AE003760, AAF56686.1, -.
PTR: A45775, A45775.
PDB: 1022, 29-NOV-99.
FlyBase, FBG00010441; pll.
InterPro; IPR000489; Death.
InterPro; IPR000719; Euk_pkinase.
DiecePro; IPR0002290; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56160 MW;
                                                                                                                                                                                                                                                                                                                                                                               EMBL; LC8476; AAA28750.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.6%;
                          Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ffam; PF00069; pkinase; 1.
Pfam; PF00531; death; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SM00005; DEATH;
                                                                                                                                                                                    DEATH domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   130
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NP_BIND
BINDING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MUTAGEN
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                                                     X-FAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART;
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                                                                                          422 K---IASDINTHVSTRVMGTFGYLAPBYAASGKLTEKSDVFSFGVVELELITGRRPVDAN 478
                                                                                                                                                                                                  525
     421
                            ----RVPENETKKNLLDYVKQQWRQNEWELLEKHLAAPMGKELDMCM 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: EXTRACEllular MALTÍX.
PIN: EXTENSINS CONTAIN A CHARACTERISTIC REPEAT OF THE PENTAPEPTIDE SER-PRO(4). THE PROLINE RESIDUE IS HYDROXYLATED AND THEN GLYCOSYLATED.
----PTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLA
                                                                                                                                                                                             479 NYYVDDSLYDDRARPLLNRASEQGDFEGLAD-AXMNNGYDREEMAR------MYA
                                                                                                                                            REGPKSLDAVVEVN-KVFGTKIYLPPEFRNFRQLSTGVDVYSFGIVLLEVFTGRQVTD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          H-A-P-P.
H-A-P-P.
2 X 7 AA TANDEM REPEATS OF T-H-R-H-A-P-P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nicotiana tabacum (Common tobacco).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-57N-1990 (Rel. 13, Created)
01-5AN-1990 (Rel. 13, Last sequence update)
16-6CT-2001 (Rel. 40, Last annotation update)
Extensin precursor (Cell Wall Aydroxyproline-rich glycoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          glycoprotein gene in lateral root initiation.";
Genes Dev. 3:1639-1646(1989).
-!- FUNCTION: HAS A SPECIALIZED STRUCTURAL FUNCTION, POSSIBLY
THE MECHANICAL PENETRATION OF THE CORTEX AND EPIDERMIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reller B., Lamb C.J.;
"Specific expression of a novel cell wall hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; S06733; S06733.
Repeat; Cell wall; Glycoprotein; Signal; Structural protein;
Hydroxylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONTAINS THE SER-PRO(4) REPEATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 X APPROXIMATE TANDÉM REPEATS.
641DD2278AB28524 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 360; DB 1; Length 62
Pred. No. 2.1e-07;
9; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        620 AA.
                                                                                                                                                                                                                                                                                                  549
                                                                                                                                                                                                                                                                                                                                              469 CAIEAGLHCTALDPODRPSMNAVLKRFE 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                CAAA----CVRHSARRRPRMSQIVRALE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTENSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-cv. Xanthi; TISSUE-Leaf;
MEDLINE-90128263; PubMed-2612909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65406 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X13885; CAA32090.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 36.6
Matches 97; Conservative
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620
73
73
242
242
235
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14;

Gaps

94;

4 APSPGTGSPPSPSNSTTTPPPASAPPTTPSSPPPSIIPTSPPSSRSTPSAPP-S 62	63 PPTPSTPGSPPPJPQPSPPAPTTPGSPPAPTRNPPPSVPGPPSNPSREGGSPRPPS 122   1   1   1   1   1   1   1   1   1	123 -SPSPPSPSSDGLSTGVVGIALGGVALLVIVI-JCLLCKKKRRDEEDAYVPPPPPP- 179 	180PGPKAGGPYGGQQQWRQQNATPPSDHVVTSLPPPKAPSPPR-OPPPPPPPP 231   1   1   1   1   1   1   1   1   1	232 PMSSSGGSDYSDRPVLPPPSP 252 
Qy Db	Qy Gö	. Qy Db	₹ - da	QQ.

Search completed: July 2, 2003, 15:22:46 Job time: 28 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 15:16:13; Search time 73 Seconds (without alignments) 1181.002 Million cell updates/sec JulyRun on:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST.....REMEMGKIKRTGQGYSGPSL 647 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapert 3.5 Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:\* A\_Geneseq\_101002:\*

/SIDS2/gogdata/geneseg/genesegp-embl/AA1980.DAT:\*/SIDS2/gogdata/geneseg/genesegp-embl/AA1990.DAT:\* /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:\*/SIDS2/gcgdata/geneseqp-emb1.AA1984.DAT:\*/SIDS2/gcgdata/geneseqp-emb1.AA1986.DAT:\*/SIDS2/gcgdata/geneseqp-emb1/AA1986.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-emb1.AA1988.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-emb1.AA1988.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-emb1.AA1988.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-emb1.AA1988.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-emb1.AA1988.DAT:\*/SIDS2/gcgdata/geneseq/geneseqp-emb1.AA1988.DAT:\*/SIDS2/gcgdata

| SIDS2/gcgdata/genesec\_genese 221: ... 220: ... 221

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Brassica napus PER	Herbicidally activ	Arabidopsis thalia	Herbicidally activ	Protein encoded by	Herbicidally activ	Herbicidally activ	Protein encoded hy	Herbicidally activ	Herbicidally activ
	DI	AAB74205	ABB92424	AAG15453	ABB92421	AAB74207	ABB91790	ABB91291	AAB74208	ABB93235	ABB92360
	93	22	23	21	23	22	23	23	22	23	23
	Match Length DB ID	647	652	544	694	633	633	669	674	674	700
% Query	Match	9.66	85.0	65.5	9.09	50.6	50.6	50.1	48.9	48.9	48.8
	Score	3440	2936,5	2260.5	2093.5	1748.5	1748.5	1729	1687	1687	1683.5
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## ALIGNMENTS

Proline-rich extensin-like receptor kinase; PERK; resistance; AAB74205 standard; protein; 647 AA. Brassica napus PERK1 protein. L8-AUG-2000; 2000WO-CA00966. 99US-0149466. 99US-0159122. (first entry) WPI; 2001-244305/25. Goring D, Silva N; (GORI/) GORING D. (SILV/) SILVA N. Brassica napus. WO200114563-A1. 19-AUG-1999; 13-CCT-1999; 17-MAY-2001 01-MAR-2001. AAB74205; plant. RESULT 1 

New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen

Herbicidally active polypeptide SEQ ID NO Herbicidal; plant; agriculture; herbicide.

Arabidopsis thaliana

WO200210210-A2 07-FEB-2002 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892.

ä

Weidler

Tietjen K,

(FARB ) BAYER AG.

WPI; 2002-269010/31.

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Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms -
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 producing transgenic plants with increased wounding
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                                                                                                                                                                                                                                                                                                         YSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEV
                                                                                                                                                                      MSSAPSPGIGSPPSPPSNSTITTPPPASAPPPTTPSSPPPSIIPTSPPPSSRSTPSAPP
                                                                                                                                                                                                       PSPPTPSTPGSPPPLPQPSPPAPTTFGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                      The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and parhogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide
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                                                                                                                                          647;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 3440; DB 22;
Pred. No. 4e-181;
0; Mismatches 2;
                        Claim 30; Fig 1; 91pp; English.
                                                                                                                                      99.68;
                                                                                                                                           Local Similarity ...
         resistance
                                                                                                    function directly.
                                                                                                                     647 AA;
 Ö
        pathogen
resistance,
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Claim 5; SEQ ID NO 1635; 261pp + Sequence Listing; English.

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12
The invention relates to identifying target proteins comprising aligning and comparing nucleic acid or mains acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 23; Length 652;
                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                  85.0%; Score 2936.5; DB 2:87.0%; Pred. No. 1.7e-153; ive 24; Mismatches 41;
                                                                                                                                                                                                                                                   574; Conservative
                                                                                                                                           useful as herbicides.
                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                652 AA;
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Best Local S
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652

Protein;

(first entry)

31-MAY-2002

ABB92424;

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ABB92424

ABB92424 RESULT

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	18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 18-JUN-1999; 21-JUN-1999; 23-JUN-1999; 23-JUN-1999; 24-JUN-1999; 25-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 26-JUN-1999; 27-JUN-1999; 28-JUN-1999; 28-JU
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413 DFKEPAKVADFGLAKIASDTNITHVSIRVMGTFGYLAPEYAASGKLITEXSDVFSFGVVLLE 472 468 LITGRRPVDANNYYDDSLVDWARPELARASEQGDFBGLADAKANNGYDREEMARNVACA 527 111111111111111111111111111111111111	MANIS433 standard; Protein; 544 AA.     MANIS433 standard; Protein; 544 AA.     MANIS433 standard; Protein; 544 AA.     MANIS433;     17-CXT-2000 (first entry)     Arabidopsis thaliana protein fragment SEQ ID No: 15711.     Proceding identification: signal transduction pathway;     Protein identification: signal     P
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169 173 228

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401

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288 YVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLV 347
                                                                                                                                                                                                                          DFKFEAKVADFGLAKIASDINIHVSTRVMGTFGYLAPEYAASGKLIEKSDVFSFGVVLLE 467
                                                                                                                                                                                                                                                                                             1 MSSAPSPGT---GSPPSPPSNSTTTTPPPA--SAPPPTTPSSPPP-PSTIPTSPPPSSRS
                                           55 TPSAPPPSPPTPSTPGSPPPLPQPSPPAPTTPGSPPAPVTPPT-RNPPPSVPGPPSNPSR
                                                                              61 PPSLPPPSPPSPTGSLT----PPLPQPSPSPTTP-SPPSPTTPSNPRSPPSPUTPS-
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                                                                                                                                          DAYYVPPPPPPPRAGGPYGGQQQWRQQNATPPSD-HVVTSLPPPPRAPSPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms.
                  Gaps
                  23;
                  Indels
        Pred. No. 1.8e-116;
'; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidally active polypeptide SEQ ID NO 1632.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Herbicidal; plant; agriculture; herbicide
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83.38; Pr. 27;
                                                                                                                                                                                                                                                                                                                                                                                      ABB92421 standard; Protein; 694
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                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana.
       Best Local Similarity
Matches 449; Conserv
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9905-015139,

9905-0155458

9905-0155458

9905-0157117

9905-0157117

9905-0157117

9905-0157132

9905-015965

9905-0159294

9905-0159294

9905-0159294

9905-0159294

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9905-0161359
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990S-0148341.
990S-0148565.
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990S-0149426.
990S-0149722.
990S-0149929.
990S-01499029.
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99US-0151065.
99US-0151066.
99US-0151066.
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990S-0151438.
990S-0151930.
990S-0152363.
990S-0153070.
                    99US-0147416
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99US-0161993.
99US-0162142.
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99US-0154039
                06-AUG-1999;
09-AUG-1999;
10-AUG-1999;
11-AUG-1999;
12-AUG-1999;
13-AUG-1999;
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16-AUG-1999;
17-AUG-1999;
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27-AUG-1999;
27-AUG-1999;
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30-AUG-1999;
31-AUG-1999;
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15. SEP-1999;
16. SEP-1999;
20. SEP-1999;
23. SEP-1999;
24. SEP-1999;
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21-0CT-1999;
21-0CT-1999;
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21-0CT-1999;
22-0CT-1999;
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20-AUG-1999;
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25-AUG-1999;
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07-SEP-1999;
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28-0CT-1999;
29-0CT-1999;
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08-0CT-1999;
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13-0CT-1999;
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22-OCT-1999;
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14-0CT-29
14-0CT-19
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Length 544;

(first entry)

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Proline-rich extensin-like receptor kinase; PERK; resistance;
                         Protein encoded by Arabidopsis gene #2.
                                                                          Arabidopsis thaliana
       17-MAY-2001
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Best Local S
Matches 363,
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(SILV/)
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                  The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are useful as herbicides.
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                                                                                                                                                                  Gaps
                                                                                                                                                                 90;
                                                                                                                                             DB 23; Length 694;
SEQ ID NO 1632; 261pp + Sequence Listing; English.
                                                                                                                                                                112; Indels
                                                                                                                                                                                                                                                                                                                          237 FVLLVALALIFFLCKKKRRRDNE-----APPAP----
                                                                                                                                         Score 2093,5; DB 2
Pred. No. 3.2e-107;
7; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSEGQTIREMEMGKIKRTGQGY 642
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63.5%;
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                                                                                                                                                    Similarity
                                                                                                                       694 AA;
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Matches 433;
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  Claim 5;
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standard; protein; 633

AAB74207

RESULT

AAB74207 ID AAB7 XX AC AAB7 XX

AAB74207

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RDEEDAYYVPPPPPPPPRAGGP---YGGQQQWRQQNAIPPSDHVVISLPPPPRAPSPPR 222
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                                                                                                                                                                                                                                                                                                                                                                                     New proline-rich, extensin-like receptor kinase nucleic acids and polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased wounding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPTPSTPGSPPPLPQPSPPAPTTPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPR--P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 633
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56.8%; Pred. No. 2.5e-88;
ive 78; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Examples; Fig 12; 91pp; English.
                                                                                                                                          99US-0149466.
                                                                                             18-AUG-2000; 2000WO-CA00966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or pathogen resistance
                                                                                                                                                                                                                                                                                                                                     WPI; 2001-244305/25
                                                                                                                                                                                                                                                                                          Silva N;
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WO200114563-A1
                                                                                                                                          19-AUG-1999;
13-OCT-1999;
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IADGQRMLVYEFVFNKTLEYHLEGKNLPVMEFSTRLRIALGAAKGLAYLHEDCHPRIIHR
                                                              FSFGVVLLELITGRRPVDANNVYVDJSLVDWARPLLNRASEQGDFBGLADARMNNGYDRE
                                 Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                     OIKASNI LIDFKFEAKVADFGLAKIASDINTHVSTRVMGIFGYLAPEYAASGKLTEKSDV
                                                                                                     EMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDINEGMRPGQSNVTSSYGGSTDY
                                                                                                                 Length 633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; SEQ ID NO 1001; 261pp + Sequence Listing; English.
                                                                                                                                                            SQTSYNADMKKFRQIALSSQEFPVSDCGTSSNDSRDMG 625
                                                                                                                                               DSSQYNEDMKKFRKMALGTQEY---NATGEYSNPTSDYG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
                                                                                                                                                                                                                                                                                        SEQ ID NO 1001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50.6%; Score 1748.5; DB 56.8%; Pred. No. 2.5e-88;
                                                                                                                                                                                                                                                                                                            agriculture; herbicide
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                                                                                                                                                                                                                                                                                   Herbicidally active polypeptide
                                                                                                                                                                                                                       ABB91790 standard; Protein; 633
                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001WO-EP09892
                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2001; 2001WO-EP09892.
                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                               thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Weidler
                                                                                                                                                                                                                                                                                                           plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                   WO200210210-A2.
                                                                                                                                                                                                                                                              31-MAY-2002
                                                                                                                                                                                                                                                                                                        Herbicidal;
                                                                                                                                                                                                                                                                                                                            Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                        07~FEB-2002
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PPTPSTPGSPPPLPQPSPPAPTTPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPR--P 120
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                                                                                                                                                                                                                                                                                                          IAGAKRLLVYEFYPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGJSYLHEDCNPKIIHR 398
                                                                                                                                                                                                                                                                                                                                                                           458
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                           PPN-SSNNSPSPPSQGGGGERGNGGNNGGNDTPPSRGSPPS---PPSRSNGDNGGSRSSP
                                                             PS-----SPSPPSP--SSDG----LSTGVVVGIAIGGVALLVIVTLICLLCKKKRR
                                                                                  120 PGDTGGSRSDNPPSSGGSSGGGGGRSNTWIALIVGVLVGAGLLMIVLIIVCLRRKKRRR
                                                                                                                      RDEEDAYYVPPPPPPPPRAGGP---YGGQQQQWRQQNATPPSDHVVISLPPPPRAPSPPR
                                                                                                                                                   180 ----DSFY-----PEPMRGNQYQYYGNNNNNASQNY--PNWHINSQGQNQQSTGGWGG
                                                                                                                                                                                                                                              NILGQGGFGYVHKGVLPSGKEVAVRQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                   223 OPPPPPPPPFMSSSG--GSDYS--DRPVLPPPSPGLVLGFSKSTFIYEELARAINGFSEA
                                                                                                                                                                                                    FSFGVYLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIKASNILIDFKFERKVADFGLAKIASDINTHVSTRVMGTFGYLAPEYAASGKLTEKSDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMARMVACAAACVRHSARRPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSSQYNEDMKKFRKMALGTQEY---NATGEYSNPTSDYG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SQTSYNADMKKFRQIALSSQEFPVSDCEGTSSNDSRDMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidally active polypeptide SEQ ID NO 502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Herbicidal; plant; agriculture; herbicide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB91291 standard; Protein; 699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-269010/31.
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15

Gaps

47;

151; Indels

78; Mismatches

363; Conservative

Matches

g õ

62 9

SAPSPGTGSPPSPPSNSTTTTPPPASAPPPTTPSSFPPPSTIPTSPPPSSRSTPSAPPPS SAPPINSTSSPSPRSNTNSTTSSP---PAPSPPSTPPQGDSSSSPPDSTSPPAPQADN

526

(first entry)

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Proline-rich extensin-like receptor kinase; PERK; resistance;
                                           Protein encoded by Arabidopsis gene #3.
                                                                                                                                                18-AUG-2000; 2000WO-CA00966
                                                                                        Arabidopsis thaliana
                                                                                                                                                                                                                                         WPI; 2001-244305/25
                                                                                                          WO200114563-A1
                                                                                                                                                                                            (GORI/) GORING
                                                                                                                                                                  19-AUG-1999;
                        17-MAY-2001
                                                                                                                                                                            13-OCT-1999;
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                                                                                                                                                                                                                          Goring D,
     AAB74208;
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                                    The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant are useful for identifying modulators. The identified modulators are useful as herbicides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     358 LHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVAD 417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        959
                                                                                                                                                                                                                                                                                                              2 SSAPSPGIGSPPSPPSNS--ITTTPPPA-----SAPPPTTPSSPPPPSTIPTSPPP---
                                                                                                                                                                                                ENSSDGSSSSSPPPPSDSSQSQSPPP-PSTSPPQQSDNNGNKGNNENNKGNDGSSGDG
                                                                                                                                                                                                                                                              GSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSPPSSSDGLSTGVVVGIAIGG
                                                                                                                                                                                                                                                                                                  VALLVIVILICLLC---KKKRRRDEEDAYYVPPPPPPPPRAGGPYGGQQQWRQQNATPP
                                                                                                                                                                                                                                                                                                                                                                            SD---RPVLPPPSPGLVLGFSKSTFTYEELARATMGFSEANLLGQGGFGYVHKGVLPSGK
                                                                                                                                                                                                                                                                                                                                         -----KAPSPPR----SPPPPPPPFMSSSGG-----SDY
                                                                                                                                                                                                                                                                                                                                                                                                                          NNVYVDDSIVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMVACAAACVRHSARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RPRMSQIVRALEGNVSLSDLNEGHRPGQSNVYSSYGGSIDYDSSQYNEDMKKFRKMALGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                       Length 699;
                  SEQ ID NO 502; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QEYNATGEYSNPISDYGLYPSGSSSEGQTTRENEMG----KIKRTGQG
                                                                                                                                                                        Indels
                                                                                                                                                   Score 1729; DB 23;
Pred. No. 3.3e-87;
3; Mismatches 167;
                                                                                                                                                                                                                            ---SSRSTPSAPPSPPTPSTPGSPPFLPQPSPPAPT-
                                                                                                                                                                     83;
                                                                                                                                                   50.1%;
                                                                                                                                                                      Conservative
                                                                                                                                                            Similarity
                                                                                                                                 699 AA;
                                                                                                                                                                   Matches 372;
 organisms
                                                                                                                                 Sequence
                  Claim 5;
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                                                                                                                                                 Query Match
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SILVA N.

Silva N;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
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                                                    Wounding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 VDSSPAPET-SNGTPPSNGTS---PSNESSPPTPPSSPPPSS---ISAPPDDISASFSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPP-------SVPGPPSNPSR---EGGSPRPPSSPSPSSDGLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              119 TPPSPGANDDRNRTNGGNNNRDGSTPSPPSSGNRTSGDGGSPSPPRSISPPQNSGDSDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   192 QQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----TPQDHVV-NMAGQGGGNWGPQQPVSGP-----HSDASNLTGRTAIPSPQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
         and
                                                                                                                                                            The present invention relates to proline-rich extensin-like receptor kinase (PERK). The PERK nucleic acids and polypeptides are useful for increasing the resistance of plants to wounding and pathogens. These are also useful for producing transgenic plants with increased wounding and pathogen resistance compared with a wild type plant, as well as in assays for identifying and developing compounds to inhibit and/or enhance polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114;
New proline-rich, extensin-like receptor kinase nucleic acids polypeptides useful for increasing plant wounding or pathogen resistance, or for producing transgenic plants with increased
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 674;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               48.9%; Score 1687; DB 22;
51.8%; Pred. No. 6.3e-85;
ive 87; Mismatches 142;
                                                                                                                  Examples; Fig 13; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                 resistance, or for prod
or pathogen resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
ses 368; Conserv
                                                                                                                                                                                                                                                                                                                                                                                  674 AA;
                                                                                                                                                                                                                                                                                                                                      function directly
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protein; 674 AA.

AAB74208 standard;

AAB74208 ID AAB7 XX

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420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                        YVDDSLVDWARPLLINRASEGGDFEGLADAKMNNGYDREEMARMVACAAACVRHSARRRPR
                                                                                                                                                            MSQ-----IVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKK
GEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWS
                                                ---NPKIIHRDIKASNILIDEKFEAKVADFGL
                                                                                             AKIASDINTHVSTRVMGTFGTLAPEYAASGKLIEKSDVFSFGVVILLELITGRRPVDANNV
                                                                                                                                                                                                                                                 640
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                                                                                                                                                                                                                                         590 FRKMALGTQEYNATGEYSRPTSDYGLYPSGSSSEGQTTREMEMGKIKRTGQ
                                                                                                                                                                                                                                                          SEQ ID NO 2446; 261pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                     Herbicidally active polypeptide SEQ ID NO 2446.
                                                                                                                                                                                                                                                                                                                                                                                                                              Herbicidal; plant; agriculture; herbicide
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                                                                                                                                                                                                                                                                                                                               ABB93235 standard; Protein; 674
                                              TRLKIALGSAKGLSYLHEDC-
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                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful as herbicides
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Length

DB 23;

48.9%; Score 1687;

Query Match

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                                       ---PTRN
                                                                                                                                           GWWGIAIGGVALLVIVTLICLLCKKKRRRDEEDA----YYVPPPPPPPPAA-GGPYGGQ
                                                                                                                                                                                            229 -----TPQDHVV-NWAGQGGGNWGPQQPVSGP-----HSDASNLTGRTAIPSPQ
                                                                                                                                                                                                                                 -AATLGHNOSTFTIDELSIATEGFAQSNLLGGGGGTVHKGVLPSGKEVAVKSLKLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSSAPSPGTGSPPSPSSNSTTTTPPPASAPPPTTPSSPPPPSTTFTSPPPSSRSTPSAPP
                                                                             --SWEGPPSNPSR---EGGSPRPPSSPSPPSPSDGLST
                                                                                                                192 QQQWRQQNATPPSDHVVTSLPPPRKAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPS
                                                                                                                                                                                                                                                                      YVDDSLYDWARPLLNRASEQGDFEGLADAKMNGYDREEMARMYACAAACVRHSARRRPR
                                                                                                                                                                                                                                                            GEREFQAEVELISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWS
                                                                                                                                                                                                                                                                                                                                                                                     252 PGLVLGFSKSTFTYEELARATNGFSEANLLGGGGFGYVHKGVLPSGKEVAVKQLKVGSGQ
                                                                                                                                                                                                                                                                                                TRLKIALGSAKGLSYLHEDC-------NPKIIHRDIKASNILIDFKFEAKVADFGL
                                                                                                                                                                                                                                                                                                                                                                                                                MSQ------IVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKK
            114;
                                                                PSPPI----PSTPGSPPPL----PQ----PSPPAP--TTPGSPPA-PVTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGQTUREMEMGKIKRTGQ
           Indels
 ed. No. 6.3e-85;
Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              active polypeptide SEQ ID NO 1571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Herbicidal; plant; agriculture; herbicide
  Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A.A.
          87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      700
51.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB92360 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
 Similarity
                                                                                                     100 PPP---
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The invention relates to identifying target proteins (ABB90790-ABB34016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value sequences are stactor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKRLLVYEFVPNNNEELHLHGEGRPTMEMSTRLKIALGSAKGLSYLHEDCNPKIIHRDIK 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASNILIDFKFEBAKVADFGLAKIASDINTHVSTRVMGTFGYLAPEXAASGKLTEKSDVFSF 461
                                                                                                   Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 PPASAEFPTTPSSPPPSTIPTSPPPSSRSTPSAPPPSPPTPSTPGSPPLPQPSPPAPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GL-----STGVVVGIAIGGVALLVIVTLICLLCKKKRRDEEDAYYVPPPPPGPKA
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                                                                                                                                                                                                                                                                                                                                                                                     ; Score 1683.5; DB; Pred. No. 1e-84; 80; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                   48.88;
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Best Local Similarity 49.2
Matches 353; Conservative
                                                                                                  Identifying plant target
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                                          Weidler
                                                                      WPI; 2002-269010/31
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               (FARB ) BAYER
                                          Tietjen X,
                                                                                                                                                                          Claim 5;
                                                                                                                                                                                                                                                                                                                                                      Sequence
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Length 700; Indels 139;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 PGPKAGGPYGGQQQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPFMSSSGGS 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying target proteins (ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using suitable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant are useful for identifying modulators. The identified modulators are useful as herbicides.
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582 QYNEDMKKFRKMALGTQEYNATGETSNPTSDYGLYPSGSSSEGQTTREMEMGKIKRTG 639
             1 MSSAPSFGIGSPPSPSSNSTTTTPPPASAPPPTTPSSPPPPSTTTTSPPPSSRSTPSAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 PPSSPSPPSPSDGLSTGVVVGIAIGGVALLVIVTLICLLCKKKRRRDEEDAYYVPPPPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23; Length 509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 5; SEQ ID NO 1634; 261pp + Sequence Listing; English.
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83;
                                                                                                                                                                       ID NO 1634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.5%; Score 1569.5;
53.2%; Pred. No. 1.3e
ilve 45; Mismatches
                                                                                                                                                                                            Herbicidal; plant; agriculture; herbicide
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                                                                                           509
                                                                                                                                                                       polypeptide
                                                                                        ABB92423 standard; Protein;
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                                                                                                                                            (first entry)
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                                                                                                                                                                   Herbicidally active
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSS
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300 VWYNGLAVUSGDGSERETARDARVEISSTATISTERIA   359   360 PWYNGLAVUSGDGSERETARDARVEISSTATISTERIA   351   361   362	VY Z4U DYSDKPVLPPPSPSPELVLGFSKSTFTYBELARATNGFSBANLLGGGGFGYVHKGVLPSGKE 299  Db 160	XX SS	Sequence 710
204 WWYNGLKWGSRAGERENDORFNIEDCHRINKUNSTHINTTHINTHINTHINTHINTHINTHINTHINTHINTHI	VAVKQLKVGSQQSEREFQAEVELISRVHHRHUVSLVGYCIAGAKRLLVYEFVPNNNLELH		Query Match Best Local Similan
260	VAVKQLKVGSAQGEKEFQAEVNIISQIHHRNLVSLVGYCIAGAQRLLVYEFVPNNTLEFH		'n
264 id8x032PitCHRSTALLANDANSSRG[STHERNCHTHIN]   11111111111111111111111111111111111	LHGEGRPTMEWSTRLXIALGSAKGLSYLHEDONPKIJHRDIKASNILLDFKFEAKVADFG	δο	2 SSAPSI
120   DAKTANDENNINGSTREAMPRICEAPENDAGGATERSONYSCOVILEITIONPENDANN 353   420   DAKTANDENNINGSTREAMPRICEAPENDAGGATERSONYSCOVILEITIONPENDANN 353   420   VATOLESTREAMPRICEAPENDAGGATERSON CAMACOVILEITIONPENDANN 353   420   VATOLESTREAMPRICEAPENDAGGATERSON PROCESSOR SEGGET SEGGET PROCESSOR SEGGET	264 LHGKGRPTMEWSLRLKIAVSSSKGLSYLHENCNPKIIHRDIKAANILIDFKFEAKVADFG	<u>a</u>	27 SA
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### VANDES,VUMARRILLY,VOMALESSNEGLOPERSLADAKONGYDERSDAMPCAAACONG 539  ### VANDES,VUMARRILLY,VOMALESSNEGLODEKIANSWINGTDERSDAMPCAAACONG 539  ### VANDES,VUMARRILLY,VOMALESSNEGLADIKIANSET,DEEDAKANGAACONG 539  ### VANDES,VUMARRILLY,VOMALESSNEGLADIKIANSET,DEEDAKANGAACONG 539  ### VANDES,VUMARRILLY,VOMALESSNEGLADIKIANSET,DEEDAKANGAACONG 539  ### RAGOVENTEAR/SESSNEGLADIKIANSET,DEEDAKANGAACONG 539  ### RAGOVENTEAR/SESSNEGLADIKIANSET,DEEDAKANGAACONG 539  ### RAGOVENTEAR/SESSNEGLADIKIANSET,DEEDAKANGAACONG 539  ### AB391536  ### RAGOVENTEAR/SESSNEGLADIKIANSET,DEEDAKANGAACONG 509  ### AB391536  #	324 LAKIALDINTHVSTRVMGTFGYLAPEYAASGKLTEKSDYYSFGVVLLELITGRRPYDANN	<u>අ</u>	
### WYDOSCYNDANDILOGIESNYPROLIDIKINEEDREEDRANDKANGUNETHERE 413  ###################################	480 VYVDDSLVDWARPLLNRASEOGDFEGLADAKMINGYDREEMARWVACAAACVRHSARRRP	රී සි	
S40 MeQUIVARIENTENDENDENDENDENDENDENDENDENDENDENDENDENDE	384 VYADOSLVDWARPLLVQALEESNFEGLADIKLNNEYDREEMARWVACAAACVRYTARRRP		105
600 INNIGENSENTIAL PROGRESSENCY   163     434	RMSQTYRALEGNYSLSDLNBGNRPGGSNYYSSYGGSTDYDSSQYNBDMKKFRKMALGTQE 	경 음	
Name	ENAIGEYSNPISDYGLYPSGSSSEGQITREMEMGKIKRIGQGYSGPSL 647	Qy	
Db         313           Qy         267           Db         345           Qy         327           Db         465           Qy         447           Db         525           Qy         567           Db         585           Qy         567           Db         585           Qy         627           Qy         627           Db         645           Qy         627           Qy         627           Qy         627           Qy         623           XX         ABB91504	TOTAL	Qy	
Ambabl2556 standard; Protein; 710 AA.	7	đ	313
Herbicidally active polypeptide SEQ ID NO 747.  Herbicidally active polypeptide SEQ ID NO 747.  Herbicidally plant; agriculture; herbicide.  Arbidopsis thaliana.  MO205210210-A2.  07 447  07-EB-2002.  28-AUG-2001; 2001WO-EP09892.  CAPA AGRAPA  Tietjan K, Weidler M;  WPI; 2002-269010/31.  Identifying plant trayet proteins for herbicidally active compounds, pbb 588 from polyments and comparing nucleic acid or amino acid sequences from non-plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant organisms - The invention relates to identifying target proteins from plant organisms and comparing and comparing nucleic acid or amino acid sequences from plant organisms and amino acid sequences from plant organisms and comparing sequences from non-plant organisms using sultable search parameters, where plant sequences from plant organisms using stateble search parameters, where plant sequences having an e-value of most similar non-plant properties are selected. The polypeptides or nucleic acid or nucleic acid sequences are selected. The polypeptides or nucleic acids enongling them are useful for identified modulators are are selected. The polypeptides or nucleic acids enongling them  AR Herbicidal and comparating modulators. The identified modulators are are selected. The polypeptides or nucleic acids enongling them	AB391536 standard; Protein; 710	δŏ	
Herbicidally active polypeptide SEQ ID NO 747.  Herbicidally plant; agriculture; herbicide.  Arabidopsis thaliana.  Arabidopsis thaliana.  MO205210210-A2.  O7 FEB-2002.  28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  CRABB ) BATER AG.  Tietjen K, Weidler M;  WPI; 2002-269010/31.  Identifying plant trayet proteins for herbicidally active compounds, pb 645 polyperising aligning and comparing nucleic acid or amino acid sequences from non-plant comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant organisms - The invention relates to identifying target proteins from plant organisms and comparing and compounds, comprising and comparing sequences from non-plant organisms and sequences from non-plant organisms using suitable search parameters, where plant sequences from non-plant organisms using suitable search parameters, where plant sequences from non-plant organisms using sequences are selected. The polypeptides or nucleic acid or and of most similar non-plant are useful for identified modulators are needed for identifying modulators. The identified modulators are acids encoding them are useful for tidentifying modulators. The identified modulators are acids encoding them	Abstract	a	
Herbicidal; plant; agriculture; herbicide.  Arabidopsis thaliana.  Arabidopsis thaliana.  Arabidopsis thaliana.  MO200210210-A2.  07 -FEB-2002. 28-AUG-2001; 2001MO-EP09892. 28-AUG-2001; 2001MO-EP09892. 28-AUG-2001; 2001MO-EP09892. 28-AUG-2001; 2001MO-EP09892. 28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP09892.  29-AUG-2001; 2001MO-EP09892.  28-AUG-2001; 2001MO-EP0982.  28-AUG-2001; 2001MO-EP0982.  28-AUG-2001; 2001MO-EP0982.  28-AUG-2001; 2001MO-EP0982.  28-AUG-2001; 2001MO-EP0982.  28-AUG-2001	3. MAI-2002 (Tirst entry)	QY	
Arabidopsis thaliana.  WO20C210210-A2.  O7-FEB-2002.  28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  CFARB ) BAYER AG.  Tietjen K, Weidler M;  WPI; 2002-269010/31.  Tedinifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant active compounds.  Claim 5; SEQ ID NO 747; 261pp + Sequence Listing; English.  The invention relates to identifying rarget proteins  Claim 5; SEQ ID NO 747; 261pp + Sequence Listing; English.  The invention relates to identifying rarget proteins  ALBB90790-ABB94015) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant organisms using by aliactor of a factor of a	<pre>"elbicidally active polypeptide SEQ ID NO Herbicidal, plant; agriculture: herbicide</pre>	qa d	
WO20C210210-A2.  07-FEB-2002. 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892. 28-AUG-2001; 2001WO-EP09892. 38-AUG-2001; 2001WO-EP09892. 38-AUG-2001; 2001WO-EP09892. 38-AUG-2001; 2001WO-EP09892. 38-AUG-2001; 2001WO-EP09892. 38-AUG-2001	Arabidopsis	Ğ €	
28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  (FARB ) BAYER AG.  Tietjen K, Weidler M;  WPI; 2002-269010/31.  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant from plant with nucleic acid or amino acid sequences from plant active compounds, comprising and comparing nucleic acid or amino acid sequences from plant active compounds, comprising and comparing nucleic acid or amino acid sequences from plant active compounds, comprising an amino acid sequences from non-plant organisms using a maino acid sequences from non-plant organisms using a factor of 3 than the E-value of most similar non-plant active compounds.  XX ABB91504.		8 8	
28-AUG-2001; 2001WO-EP09892.  28-AUG-2001; 2001WO-EP09892.  (FARB ) BAYER AG.  Tietjen K, Weidler M;  WFI; 2002-269010/31.  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant cryanisms -  Ciganisms -  Claim 5; SEQ ID NO 747; 261pp + Sequence Listing; English.  The invention relates to identifying target proteins  Claim 5; SEQ ID NO 747; 261pp + Sequence Listing; English.  The invention relates to identifying target proteins  (ABB90790-ABB94016) for herbicidally active compounds, comprising  Alimina acid sequences from non-plant cryanisms using  With nucleic acid or amino acid sequences from non-plant cryanisms using  Sultable search parameters, where plant sequences from non-plant cryanisms using  Sultable search parameters, where plant sequences having an E-value sequences are selected. The polypeptides or nucleic acids encoding them  Sequences are selected. The polypeptides or nucleic acids encoding them  Example 1 and		. 음 	
(FARB ) BAYER AG.  Tietjen K, Weidler M;  WPI; 2002-269010/31.  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant cryanisms - cryanisms using with nucleic acid or amino acid sequences from non-plant organisms using cryanisms using cryanism cryanism cryanisms using cryanisms using cryanism cryanisms cryanisms using cryanisms companisms	28-AUG-2001;	ŏ	
Tietjen K, Weidler M;  WPI; 2002-269010/31.  Gov E27  Identifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant with nucleic acid or amino acid sequences from non-plant  Claim 5; SEO ID NO 747; 261pp + Sequence Listing; English.  The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences having an E-value with nucleic acid or amino acid sequences having an E-value of most similar non-plant as sequences are selected. The polypeptides or nucleic acids encoding them XX sequences are selected. The identified modulators are lasting for identifying modulators. The identified modulators are	28-AUG-2001;	' 셤	
Tietjen K, Weidler M;  WPI: 2002-269010/31.  Gy 627  Identifying plant target proteins for herbicidally active compounds, comprising and comparing nucleic acid or amino acid sequences from non-plant from plant with nucleic acid or amino acid sequences from non-plant seguence Listing; English.  The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally acitive compounds, comprising XX aligning and comparing nucleic acid or amino acid sequences from plant organisms using with nucleic acid or amino acid sequences from plant organisms using xistable search parameters, where plant sequences having an E-value xistable search parameters, where plant sequences having an E-value xistable search parameters, where plant sequences having an E-value xistable search parameters, where plant sequences are selected. The polypeptides or nucleic acids encoding them xistable search parameters are selected. The polypeptides or nucleic acids encoding them xistable search parameters are selected. The identified modulators are lastin for identifying modulators. The identified modulators are	(FARB	γQ	
Tdentifying plant target proteins for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from non-plant plant with nucleic acid or amino acid sequences from non-plant plant with nucleic acid or amino acid sequences from non-plant plant with nucleic acid or amino acid sequence Listing; English.  The invention relates to identifying target proteins  (ABB91504)  The invention relates to identifying target proteins  (ABB910790-ABB84016) for herbicidally active compounds, comprising  ABB91504;  ABB91504;  AN  ABB91504;  AN  AN  ABB91504;  AN  AN  ABB91504;  AN  ABB91504;  AN  AN  AN  ABB91504;  AN  AN  AN  ABB91504;  AN  ABB91504;  AN  AN  ABB91504;  AN	Tietjen K, Weidler	g q	
Identifying plant target proteins for herbicidally active compounds, from plant with nucleic acid or amino acid sequences from non-plant from plant with nucleic acid or amino acid sequences from non-plant screens are selected. The invention relates to identifying target proteins (ABB90790-ABB94105) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant prant sequences from plant with nucleic acid or amino acid sequences having an E-value with nucleic by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them xx are useful for identifying modulators. The identified modulators are		Qy	Ę
Claim 5; SEQ ID NO 747; 261pp + Sequence Listing; English.  The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising ALIGHARD ABB94016) for herbicidally active compounds, comprising with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from plant squences from non-plant organisms using stable search parameters, where plant sequences having an E-value Squences are selected. The polypeptides or nucleic acids encoding them XX Herbicida XX Herbicida XX Herbicida		Db	593 S
The invention relates to identifying target proteins (ABB90790-ABB94016) for herbicidally active compounds, comprising aligning and comparing nucleic acid or amino acid sequences from plant with nucleic acid or amino acid sequences from non-plant organisms using sultable search parameters, where plant sequences having an E-value greater by a factor of 3 than the E-value of most similar non-plant sequences are selected. The polypeptides or nucleic acids encoding them are useful for identifying modulators. The identified modulators are	Claim 5;	ABB D	91504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43.9%; Score 1515.5; DB 23; Length 710; arity 46.2%; Pred. No. 1.7e-75; onservative 81; Mismatches 158; Indels 149; Gaps
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46.4%; Pred. No. 3e-72;
ive 87; Mismatches 158;
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Mismatches 127; Indels 225;
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Db 703 LYSGNYSAKSSSD 715	New proline-rich, extensin-like receptor kinase nucleic acids and
505 EYSNPTSDYGLYPSGSSSE	X WPI; 2001-244305/25.
Db 652 VRALDCDGDSGDISNGIKIGQ	X Goring D, Silva N;
Qy 545 VRALEGNYSLSDLNEGMRPGQSNVYSSYG	A (GORI/) GORING D. A (SILV/) SILVA N.
QY 485 SLVDWARPLINRASEQGDFEGLADAKANN	PR 19-AUG-1999; 99US-0149466. PR 13-OCT-1999; 99US-0159122. XX
532	X 18-AGG-2000; 2000WO-CA00966. X
Qy 425 SDTWTHVSTRVMGIFGYLAPEYAASGKLJ	X 01-MAR-2001.
Db 472 GLAYTHEDCHPKIHRDIKSANILLDDG	
OY 383 GLSTLHEDCNPKIIHRDIKASNILIDEKI	X S Arabidopsis thaliana.
Db 419 ISRVHHRHLVSLVGYCISDQHRLLIYEY	<pre>W Proline-rich extensin-like receptor kinase; PERK; resistance; W plant.</pre>
QY 323 ISRVHHRHLVSLVGYCIAGAKRLLVYEF	E Protein encoded by Arabidopsis gene #1. $_{ m X}$
Db 359 FSYEELAEITQGFARKNILGEGGFGCVY	DT 17-MAY-2001 (first entry)
Qy 263 FIYEELARATNGFSEANLLGQGGFGYVH	AC AAB74205; XX
326	Anb.4206 ID AAB74206 standard; protein; 731 AA. XX
DD Z bB RRKKRNIDSYNHSQYLPHPNFSVKS	RESULT IS
Qy 160 CXKKRRDEEDAYYVPPP	54# LYNALEGNVSLEDLINGERKREGNVESYGGSTOFTDSSORNEDMIKFRKMALGOFENA 602
AY Last and the contract of th	Db 550 ESLVEWARPLIGGAIENBEFDELVDPRIGKNFIPGEMFRAVBAAAACVRHSAAKRPKMSQ 609
	QY 484 DSLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARWVACAAACVRHSARRPRMSQ 543
QY 87 GSPPAPUTRNPPPSVPGPPRNP	490 ELDLATHVSTRVMGTFGYMAPEYATSGKLSEKADVYSYGVILLELITGKRYPVPTSQPLGD
Db 89 DST-PSPPPPTSNESPSPPEDSETPPAP	
DD 29 NSALPPVDSSPPSPPADSSSTPPLSEPS  Qy 41 PSTIPISPPPSSRSTPSAPPPSF	QY 366 PIMEMSTRIKIALGSAKGLSYLHEDCNEKITERDIKASNILIDFKFERKVADFGLAKTAS 425
Oy 2 SSAPSPGTGSPPSPSNSTTT	370 KIGGSQGEREFKAEVEIISKVHHRHIVTLVGYCISEQHRLLVYDYVDNNIHHTHAFGR
Best Local Similarity 43.4%; Pred. No Matches 321; Conservative 93; Misma	Db 311 MYASSDSGMVSR-QRSWESYDELSQVISGESEKNILGEGGGFGCVYKGVLSDGREVAVKQL 369 306 KVGSGGGERESVARDFITSRVHHRHIVGTVGVCTAGARDTIJVVPPUDJANITPI UT UTDEND 266
Sequence 731 AA;	246
CC and developing compounds to inhibit a CC function directly.	QY 186 GPYGGQQQWRQQNATPBSDHVVTSLPPPPKAPSPPRQPPPPPPPSSSGGSDYSDRP 245
CC plants with increased wounding and pa	28
	SPSSDGLSTGVVVGLAIGGVALLVIVTLICLLCKKKRRRDEBDAYYVPPPPPPGPKAG
	DD 171 PPPPPATSASPPSSNPPDPSTLAPPPLEWWYPERFIDARMSTATES 200
resistance, or pathogen	111 QTVSPPPPPDASPSPPAPTTINP
PT polypeptides useful for increasing pl	QY 51PSPPTPSTPGSPPPLPQPSPAPTTPGS 88

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22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----PPPGPKAGGPYGGQQQQWRQQNATP 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SDGFLYGQDPGKGYSSGPNGSHYNNSQQQQSSM 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKST 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FVPNNNLELHLHGEGRPTMEWSTRLKIALGSAK 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ::||:
EYBAQAIMKSSFSLNLSYDCKVLVADFGLARLN 531
                                                                                                                                                                                                                                                                                                                                              -TPPPAS--------APPPTTPSSPPP 40
                                                                                                                                                                                                                                                                                                                                                               PPTPSTPGSPPP----LPQPSPPA----PTTP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------VADFGLAKIA 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTEKSDVFSFGVVLLELITGRRPVDANNYVDD 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NNGYDREEMARMVACAAACVRHSARRPRMSQI 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKRYVEHEVFRMIETAAACVRHSGPKRPRMVQV 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---STIYDSGQYNEDIMKFRKMARGGDNSVESG 702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FGGSTDYDSSQYNEDMKKFRKMALGTQEYNAIG 604
plant wounding or pathogen
enic plants with increased wounding
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                          proline-rich extensin-like nucleic acids and polypeptides istance of plants to wounding ful for producing transgenic i pathogen resistance compared s in assays for identifying it and/or enhance polypeptide
                                                                                                                                                                                                                                                                           1415.5; DB 22; Length 731;
No. 5.4e-70;
natches 156; Indels 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KFEAK-----
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Search completed: July 2, 2003, 15:22:14 Job time: 76 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 2, 2003, 14:57:12; Search time 18 Seconds (without alignments) 1057.591 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST.....REMEMGKIKRTGQGYSGPSL 647

BLOSUM62 Gapop 10.0 . Sapext 0.5 Scoring table:

262574 Total number of hits satisfying chosen parameters:

262574 seqs, 29422922 residues

Searched:

Minimum DB seq length; 0 Maximum DB seq length; 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1ssued\_patents\_AA:\*
1: /cgn2\_6/ptodata/1/iaa/5A\_CCMB.pep:\*
2: /cgn2\_6/ptodata/1/iaa/5B\_CCMB.pep:\*
4: /cgn2\_6/ptodata/1/iaa/6A\_CCMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/6B\_CCMB.pep:\*
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_CCMB.pep:\*
6: /cgn2\_6/ptodata/1/iaa/PCTUS\_CCMB.pep:\* Database :

Prec. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUNDARIES

;		dР			SUMMARIES	
Result		Query		1	1	
, PO.	Score	Match	Length DB	g :	ID	Description
-	754.5	21.9	968	4	US-09-228-986-76	Sequence 76, and
2	736	21.3	630	4	US-09-228-986-71	, ,
m	703.5	20.4	707	4	US-09-228-986-80	10
ŦŤ	678	19.8	638	4	228	Sequence 74 anni
Ŋ	604.5	17.5	1196	4	US-08-831-706-2	
9	593	17.2	903	4	US-09-228-986-78	Segmence 78. April
7	579.5	16.8	980	7	US-08-473-553A-6	· .
80	573	16.7	858	7	US-08-265-628-2	Segmence 7. Annli
O	572.5	15.6	985	7	-473	ì
10	572	16.6	857	Н	-717-3	í
11	566.5	16.4	999	4	US-09-228-986-68	- O
12	560.5	16.2	632	4	-228-986-7	Sequence 77 Appl
13	552	16.0	282	7	US-08-473-5538-4	-
편 근	545	15.8	321	٦	US-08-447-185-1	-
15	545	15.8	544	~	US-08-587-6808-25	10
16	543	15.7	655	7	228-986-70	2
17	539.5	15.6	857	Н	US-07-717-3315-3	. (*
18	525	15.2	666	7	-08	, v
19	206	14.7	712	Н	US-08-587-889-2	Seguence 2, Appli
20	206	14.7	712	ď	US-08-980-060-5	, N
21	206	14.7	712	4	US-09-307-185-5	, M
22	206	14.7	712	'n	PCI-US96-09193-2	, C
23	495	14.3	629	4	US-09-228-986-75	75
**************************************	486	14.1	739	4	US-09-503-922-1	
25	456.5	13.2	711	4	US-09-228-986-79	Sequence 79. Appl
26	430	12.5	069	4	US-09-228-986-69	69
27	393.5	11.4	1025	~	-567-	4

Sequence 4, Appli	4	Ý	Sequence 6. Appli	7.3		Ġ	Ċ	-	4	4	Sequence 4. Appli	N	32	Segmence 65 April	9	65,	
US-08-587-6835-4	US-08-475-8918-4	US-08-980-060-6	US-09-307-185-6	US-09-228-986-73	GS-08-475-891A-2	US-08-567-375-2	US-08-587-680A-2	US-08-445-640-4	US-08-170-558-4	US-08-447-314-4	US-08-445-461-4	US-08-336-343A-2	US-08-642-255-32	US-07-609-716-65	US-08-475-411A-65	US-08-478-029A-65	US-08-580-545B-6
7	~	7	4	4	N	C)	C4	М	m	m	m	Н	Н	Н	4	4	7
1025	1012	501	501	947	1023	1023	1023	913	913	913	913	919	330	408	4.08	80*	297
11.4	10.7	10.6	10.6	10.6	10.2	10.2	10.2	10.0	10.0	10.0	10.0	9.9	9.0	9.6	9.6	9.6	9.5
393.5	368	367.5	367.5	367.5	351	351	351	347	347	347	347	341	331.5	331.5	331.5	331,5	329.5
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## ALIGNMENTS

RESULT 1 US-09-228-986 ; Sequence 76 ; Patent No.	RESOLT 1 US-09-228-986-76 ; Sequence 76, Application US/09228986 : Patent No. 6359198	
GENERAL GENERAL GENERAL GENERAL		
; TITLE OF	itions Isolated from Plant Cells eir Use in the Modification of Plant Cell	Signalling
; FILE ; CURREN	FERENCE: 11000/1020 APPLICATION NUMBER: US/09/228,986	•
; CURRENT FI		
SOFTWARE:	WARE: FastSEQ for Windows Version 3.0	
; LENGIH: 968 ; TYPE: PRT ; ORGANISM: EU US-09-228-986-76	TYDG: PS TYPE: PS ORGANISM: Eucalyptus grandis 9-228-986-76	
Query Match	21.98;	
Matches	55.3%; Fred. NO. 1.28-35; vative 89; Mismatches 133; Indels 115; Gaps	16;
Qy	VALLVIVILICLLCKKKRRRDEE	169
QQ	533 PPKPFGPYYFIASPYAFPDNGGTALSKGVIVGIAIGGTVLVLGLYVLGLYALKQKKKAEK 59	592
0λ	170 DAYYVPPPPPGPKAGGPYGGQQQWRQQNAIPPSDHVVISLPPPPKAPSPPRQPP 22	225
DÞ	593 -ALELSRPFASWAPSGKDSGGAPQLKGARW	621
0y	ARATNGFSEANLLGOGG	285
qa	622	644
Οy	SGKEVAVKQLKVGSGQGEREFQAEVELISRVHHRHLVSLVGYCIAGAKRL	345
qq	645 YGKVYRGVLPDGHILAIKRAQQGSMQGATEFKTEIELLSRVHHKNLVGLIGRCFEQGEQM 70	704
Qy	STRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNI	405
QQ	GTLRDSLTGKSGIYLDWKRRLRIALGSARGLAYLHSLANPPIHRDVKSTNI	764
QY	SDINT-HVSTRVMGTFGYLAPBYAASGKLTEKSDVFSFGVV	464
qa	765 LIDEHLTAKVADFGLSKLVSDSGKGHVSTQVKGTLGYLDPEYYNSQQLTEKSDVSFGVV 82	824

465 LLELITGRRPVDANNVYVDDSLVDWARPLLNRASEQGDFEG---LADARMN-GYDREEM 520 : | | : | : | : | : | : | |

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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
ITILE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
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APPLICANT: Strabala, IImothy
APPLICANT: Strabala, IImothy
APPLICANT: Newenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 71
LENGTH: 630
MLELITAKQPIEKGKYVVRE----IRTAMDKNDQ--DYYGVREMMDPSMRSMGY-LVGF 876
                                               90 PAPVTPPTRNPPPSVPGFP---SNPSREGGSPRPPSSPSPPSPSSDGLSTGVVVGIAIGG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     147 VALLVIVTLICLICKKKKRRDEEDAYIVPPPPPGPKAGGPYGGQQQQWRQQNATPPSDH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252 AALLF-----WRRK---PQEH 274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         267 ELARAINGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLK-VGSGQGEREFQAEVEIISR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        326 VHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLE--LHLHGEGRPTMEWSTRLKIALGSAKG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 LSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKIASDINTHVSTRVMGTFGYLA 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                207 VVTSLPPPPKAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125; Indels 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 630;
                                                                                    581 SQ----YNEDMKKFRKMALGTQEYNAIGEYSNPISDYGL 615
                                                                                                       ; DB 4;
8.5e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.3%; Score 736; DS 37.2%; Pred. No. 8.5e iive 68; Mismatches
                                                                                                                                                                                          Sequence 71, Application US/09228986
Patent No. £359198
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 37.2%
Matches 175; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pinus radiata
US-09-228-986-71
                                                                                                                                                            RESULT 2
US-09-228-986-71
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Sequence 80, Application US/09228986 Patent No. 6359198 GENERAL INFORMATION:

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Sequence 74, Application US/09228986
Fearant No. 6351198
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: Ond Their Use in the Modification of Plant Cell Signalling
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
IENGTH: 638
TYPE: PRT
                                                                                                                                                                                                                                                                             -<del>1</del>
                                                                                                                                                                                                                                                                                                                                      ---- 134
                                                                                                                                                                                                                                                                                                                                                                                          135 STGVVVGIAIGGVALLVIVILICLLCKKKRRRDEEDAXXVPPPPPPPPPPGPKAGGPYGGQQQQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                               --EEKL 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248 PPPSPGLVLGFSKSTFTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKV 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         308 G--SGQGEREFQAEVELISRVHHRHLYSLYGYCIAGAKRLLYYEFVPNNNL--ELHLHGE 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 ASDINIHVSTRYMGIFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVD 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              620 QSLVRWAIPQLH-----DIDALAKMVDPALKGSYPAKSLSRFADIIALCIQPEPERRPP 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             195 WRQQNATP---PSDHVVTSLPPPPKAPSPPRQPPPPPPPFMSSSG-----GSDTSDRPVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 STLSLQRPEDFLDAVSNISRLHHENITELVGYCTEHEQYLLYVEYFDNGSLYDVLHMADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DSIVDWARPLINRASEQGDFEGLA---DAKMNNGYDREEMARMVACAAACVRHSARRPR
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                           85;
                                                                                                                                                                                                                                                                                                         84 TIPGSPPAPVIPPTRNPPPSVPGPPSNPSREGGSPRPPSSPS--PPSPSSDG-
                                                                                                                                                                                                                                   Length 707;
                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQY 583
                                                                                                                                                                                                                          20.4%; Score 703.5; DB 4; 34.0%; Pred. No. 6.8e-33; iive 81; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                       290 SGGAIVGIIFAVILTVVAAILGVIIYARKSPRREQD----
CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DENE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 80
                                                                                                                                                                                                                      Query Match
Best Local Similarity 34.0%
Matches 178; Conservative
                                                                                                                                     ; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-228-986-80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 4
US-09-228-986-74
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Sequence 78, Application US/09228986
Sequence 78, Application US/09228986
GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Niels
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 11000/1020
                                                                                                                                                                                                              1102
                                                                                      RHIVFLEGYCKVGDERLLVNEVMKYGSLEDVLQDPKKGGVKLKLSTRRKIAIGSARGLAF 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 FIYEELARATHGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEI 322
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                                                                                                                                                                                                                                                      506 LADAKMNNGYDRE-----EMARMVACAAACVRHSARRPRKSQI----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 903;
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1,7e-26;
ches 99;
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APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
                                                                                                                                                                                                                                                                                                                                                                                                     1163 GIDSOSTIRSIEDGGFSTIEMVDMSIKEVPEG 1194
                                                                                                                                                                                                                                                                                                                                                          ----VRALEG-----NVSLSDLNEG 560
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44.9%; Pred. No. 1.7e
tive 52; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/08473553A Patent No. 5859338
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US-09-228-986-78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 44.51
Matches 133; Conservative
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                                                                                                                                                                                                                                                                                                  487 VDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMVACAAACVRHSARRFRRSQIVR
                                                                                                                                                                  254 IVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYHKGVLPSGKEVAVKQLKVGS-GQG
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                                                                                                                            22;
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                                                                            Length 638;
                                                                                                                          68; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            547 ALEGNVSLSDLNEGMRPGQSNVYS-----SYGGSTDYDSS 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 678; DB 4;
Pred. No. 1.7e-31;
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Patent No. 6245969
GERRAL INFORMATION:
APPLICANT: Chong, Joane
APPLICANT: Li, Jianming
TILLE OF INVANION: Receptor Kinase BINI
FILE REPERBNOE: 07251/022001
CURRENT APPLICATION NUMBER: US/08/681,706
CURRENT FILING DATE: 1997-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
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                                                                         19.6%;
                                                                  Ouery Match
Best Local Similarity 43.1%
Matches 147; Conservative
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Pinus radiata
) ORGANISM: Pi:
US-09-228-986-74
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Best Local Simi
Matches 157;
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US-08-881-706-2
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(5)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593 PLGG---CELVFNETSFAGNTYLCLPHRVSCPIRPGQT-----SDHNHTAL 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           636 FSPSRIVITVIAAITGLILISVAIRQMNKKKNGKSLAWKLTAFQKLDFKSEDVLEC---L 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---GESKSTFTYEELARATNGF 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             276 SEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGERE--FQAEVEIISRVHHRHLVS 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 LVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394 KIIHRDIKASNILIDFKFEAKVADFGLAKIASD-INTHVSIRVMGTFGYLAPEYAASGKL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               453 TEKSDVFSFGVVLLELITGRRPVDANNYYVDDSLVDWARPL---LNRASEQGDFEGLADA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16.8%; Score 579.5; DB 2; Length 980; 34.8%; Pred. No. 1.1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                  Albritton & Herbert
Suite 3400
TITLE OF INVENTION: Transformed Plants, and Proteins NUMBER OF SEQUENCES: 11
                                                                          CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Eloppy disk
COMPUTER: IBM PC compatible
OPERATING SYSIEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 8000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                510 KMNNGYDREEMARMYACAAACVRHSARRPRMSQIVRAL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 134;
                                                                                                                                                                                                                                                                           CLASSIFICATION: 800 1330
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
RECISTRATION NUMBER: 38 304
RECISTRATION NUMBER: A-6086/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPRONE: (415) 398-3249
TELEPRONE: (415) 398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                             CORRESPONDENCE ADDRESS:
ADDRESSER: Flehr, Hohbach, Test,
STREET: Four Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 LPPPS-----PGLVL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  980 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 34.8*
Matches 139; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE; protein US-08-473-553A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CENGTH:
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Sequence 2, Application US/08265628 Patent No. 5821094 GENERAL INFORMATION:

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266 EELARATNGFSEANLLGQGGFGTVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              326 VHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGR-PIMEWSTRLKIALGSAKGL 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      385 SYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKIASDINTHVSTR-VMGTFGYLA 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PETAASGKIJEKSDVFSFGVVILELITGRRPVDANNVTVDDSLVD--WARPLINRASEQG 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          502 D---FEGLADAKHNNGYDREEMARWYACAAACVRHSARRRPRMSQIVRALEGNVSLSDLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13; Gaps
                   APPLICANT: Goring, Daphne
TITLE OF INVENTION: S-LOCUS RECEPTOR KINASE GENE IN A
TITLE OF INVENTION: SELF-INCOMPATIELE BRASSICA NAPUS LINE
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.7%; Score 575; DB 2; Le
39.6%; Pred. No. 1.7e-25;
Live 65; Mismatches 120;
                                                                                                                    McAndrews, Held & Malloy, Ltd
0 W. Madison St. Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       559 EGMRPGQSNVTSSYGGSTDYDSSQYNED 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 03-MAR-1992
ATORNEY/AGENT INFORMATION:
NAME: Pochopien Ph.D., Donald J.
REGISTRATION NUMBER: 32,167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-707-8889
TELEFAX: 312-707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/959,945
                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/265,628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US 07/847,564
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Rothstein, Steven J.
                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE; MCANDrews, Held
STREET: 500 W. Madison St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 312-707-9155
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERATICS:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM: HEDIUM IYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 16.73
Best Local Similarity 39.6
Matches 130; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-265-628-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: APPLICATION NUMBER:
                                                                                                                                            STREET: 500 W. N
CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-473-553A-2
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US-07-717-331F-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 LVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTHEWSTRLKIALGSAKGLSYLHEDCNP 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     394 KIIHRDIKASNILIDFKFFEAKVADFGLAKIASD-TNTHVSTRVMGTFGYLAPEYAASGKL 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------ SDHNHTAL 640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     187 PYGGQQQQWRQQNATPPSDHVVTSLPPPPRAPSPPRQPPPPPPPPPFMSSSGGSDYSDRPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [:|| ||:||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|
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16.6%; Score 572.5; DB 2; Length 985;

Best Local Similarity 34.6%; Pred. No. 2.7e-25;

Matches 138; Conservative 65; Mismatches 135; Indels 61.
                      APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven B.
APPLICANT: Clark, Steven B.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
NORMERS OF EXQUENCES: 11
CORRESSONDENCE ADDRESS:
ADDRESSER: Fleir, Sothach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KMNNGYDREEMARMVACAAACVRHSARRRPRMSQIVRAL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER FRANCE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   598 PLGG---OFLVENETSFAGNTYLCLPHRVSCPIRPGQT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A-60886/RFT/RMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,553A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NCHBER: A-600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 LPPPS-----PGLVL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      : California
RY: United States
94111-4187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-473-553A-2
                                                                                                                                                                                                                                                                                                                                                                       CITY: San Francisco
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      STAIE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            510
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11; 482 301 AVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHL 360 254 497 135 STGVVVGIAIGGVALLVIVILICLLCKKKRRRDEEDAYYVPPPPPPPPPRAGGPYGGQQQQ 194 255 VLGFSKSTFT----YEEL-----ARAINGFSEANLLGQGGFGYVHKGVLPSGKEV 300 361 HGEGRPT-MEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFG 419 420 LAKIASDINTHVST-RVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVDAN 478 NVYVDDSLVD--WARPLINRASEQGDFEGLADAKMNNG--YDREEMARMVACAAACVRHS 534 195 WRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPPMSSSGGSDYSDRPVLPPPSPGL 498 ----SKREFSGEYKFEELELPLIEMETVVKATENFSSCNKLGOGGFGIVYKGRILDGKEI Sequence 2. Application US/07717331F
Patent No. 5484905
GENERAL IMPORATION:
APPLICANT: June Nasrallah; Michael Nasrallah; and Joshua
APPLICANT: Stein
ITLE OF INVENTION: Encoded At The Self-Incompatability Locus
TITLE OF ENVENTION: Encoded At The Self-Incompatability Locus
CORRESPONDENCE ADDRESS:
ADDRESSE: Yahrak & Associates
STREET: 25 Skytop Drive
CITY: Trumbul
STATE: Connecticut 16.6%; Score 572; DB 1; Length 857; 32.3%; Pred. No. 2.5e-25; Indels ::| :: : : | | ::|::| 443 ASGKIISLIV-GVSVLLLLIMFC-LWKRKQXRAKASAISIAN---83; Mismatches 119; US/07/717,331F JUNEAU AND SOUTH AND SOUTH OF THE SOUTH AND SO NAME: George M. Yahwak REGISTRATION NUMBER: 26,824 TELECOMMUNICATION INFORMATION: TELEPHONE: (203)268-1951 TELEFAX: (203)268-1951 INFORMATION FOR SEQ ID NO: 2: SROUNCE CHARACTERISTICS: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy Disk COMPUTER: Macintosh : 857 amino acids amino acids Conservative 535 ARRRPRMSQIV 545 MOLECULE TYPE: peptide Connecticut: USA Query Match Best Local Similarity Matches 139; Conserv 06611 TOPOLOGY: US-07-717-331F-2 COUNTRY: LENGIH: 479

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US-08-473-553A-4
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APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nieis
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
FILE REFERENCE: 1100//1020
GURRENT APPLICATION NUBER: US/09/228,986
GURRENT FILING DAIE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
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; Settle No. 6359198
; GENERAL INPORMATION:
; APPLICANT: Strabala, Timothy
; APPLICANT: Micuwenhulzen, Niels
; TILLE OF INVENTION: Compositions Isolated from Plant Cells
; TILLE OF INVENTION: and Their Use in the Modification of Plant Cell Signalling
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Pred. No. 4e-25;
3; Mismatches 166;
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                                                                                                                                                              Sequence 68, Application US/09228986 Patent No. 6359198
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US-09-228-986-68
793 AEHRPAMSSVV
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Best Local Simi
Matches 157;
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US-09-228-986-68
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US-09-228-986-77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        310 GQGEREFQAEVEIISRVHHRHLVSLVGYCIAGARRLLVYEFVPNNNLELHLHGEGRPTME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          506 PETTYVVGTLGYIAPELIQTGKATPSSDVFSFGVLLLEVACGKSPVDS----LEDSERMI
                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                             97;
                                                                                                                                                                                                                                                                               632;
                                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 EQEYW------
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Meyerowitz, Elliot M.
APPLICANT: Clark, Steven E.
APPLICANT: Williams, Robert W.
TITLE OF INVENTION: Plant Clavatal Nucleic Acids,
TITLE OF INVENTION: Transformed Plants, and Proteins
WUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSES: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: San Francisco
STATE: California
COUNTRY: United States
2.1P: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                            ch 16.2%; Score 560.5; DB 4;
11 Similarity 31.1%; Fred. No. 8.3e-25;
133; Conservative 65; Mismatches 132;
FILE REPERENCE: 11000/1020
CURRENT APPLICATION NUMBER: 35/09/228,986
CURRENT FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 130
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/473,553A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08473553A Patent No. 5859338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                    ; ORGANISM: Pinus radiata
US-09-228-986-77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        544 IVRALEG 550
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618 VCOVLNG 624
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Best Local Similarity
Matches 133; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 SGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNN 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LELHLHGEGRPT--MEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEA 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     414 KVADFGLAKIASDIN-THVSTRVMGTFGYLAPBYAASGKLTEKSDVFSFGVVLLELITGR 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 RPVDANNYYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMVACAAACVR 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
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                                                                                                                                                                                                                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/UB537680A
Fatent No. 597434
GENERAL INFORMATION:
APPLICANT: Ronald, Pamela C.
APPLICANT: Ronald, Pamela C.
APPLICANT: Scabo, Veronique
TITLE OF INVENTION: Disease Resistance in Plants
INUMER OF ENQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
GITT: San Francisco
STAIE: California
                                                                                                                                                                                                                                                                                                      Length 321;
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                           Ouery Match
15.8%; Score 545; DB 1; I
Best Local Similarity 38.0%; Pred. No. 3.2e-24;
Matches 123; Conservative 57; Mismatches 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PATENTIN RELEASE #1.0, Version #1.35 CURRENT APPLICATION DATA:
APPLICATION NUMER: US/08/587,680A FILING DATE: 17-JAN-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/373,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             533 HSARRPPRMSQIVRALEGNVSLSD 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                           NAME: Goldman Mr., Michael L. TELECOMOUNICATION INFORMATION: TELEPHONE: (716)263-1000
TELEFAX: (716)-263-1600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                       321 amino acids
                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
                                                                                                                                                                                                                                    ; MOLECULE TYPE: peptide US-08-447-185-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94111-3834
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                                                                                                                                                LENGTH:
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Parent No. 5648599
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GEORGE
APPLICANT: Martin, Gregory B.
TITLE OF INVENTION: GENE CONFEREING DISEASE RESISTANCE
TITLE OF INVENTION: TO PLANTS BY RESPONDING TO AN AVIRGLENCE GENE IN PLANT PATHOGE NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 282 GQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGERE--FQAEVEIISRVHHRHIVSLVGYCI 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                340 AGAKRLLVYEFYPENNILELHLHGEGRPTMENSTRLKIALGSAKGLSYLHEDCNPKIIHRD 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60 NKDTNLLEYEYMPNGSLGELLHGSKGGHLQWETRHRVAVEAAKGLCYLHHDCSPLILHRD 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSFGVVLLELITGRRPVDANNVYVDDSLVDWARPL---LNRASEQGDFEGLADAKMNNGY 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         400 IKASNILIDFKFEAKVADFGLAKIASD-TNTHVSTRVMGTFGYLAPEYAASGKLTEKSDV 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                   94; Indels
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                                                                                                                                                                                                                                                                                                                                                                                    16.0%; Score 552; DB 2;
42.5%; Pred. No. 1.1e-24;
tive 53; Mismatches 94
            CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: S110A. RObin M.
REGISTARION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-60886/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1889
TELEFAX: (415) 388-3249
TELEFAX: 910 277299
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 515 DREEMARMVACAAACVRHSARRRPRMSQIVRAL 548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 PLTSVIHVFKIAMMCVEEEAABRPTMREVVHML 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Michael L. Goldman
STREET: Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/111,078
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/447,185
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
06-JUN-1995
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 42.58
Matches 116; Conservative
                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rochester
STATE: New York
COUNTRY: U.S.A.
ZIP: 14603
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                             TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                            US-08-473-553A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -447-185-1
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243 DRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAV 302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          423 IASDINI-HVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVDANNY 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    482 VDDSLVDWARPLLNRASEQGDFEGLADAKMINGYDREEMARMVACAAACVRHSARRRPRM 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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: LOCATION: 1..544
US-08-587-680A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
15.8%; Score 545; DB 2; Length 544;
Best Local Similarity 40.7%; Pred. No. 5.5e-24;
Matches 125; Conservative 59; Mismatches 111; Indels
FILING DATE: 17-JAN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/475,891
FILING DATE: 07-JUN-1995
PRIOR APPLICATION NUMBER: US 65/004,645
FILING DATE: 29-SEP-1995
FILING DATE: 29-SEP-1995
FILING DATE: 04-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bastlan, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 02070-0589400S
TELEPHONE: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ::|: |
526 REVVQML 532
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Search completed: July 2, 2003, 15:16:13 Job time : 21 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 15:13:41; Search time 35 Seconds (without alignments) 2125.726 Million cell updates/sec July Run on:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST......REMEMGKIKRTGQGYSGPSL 647 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

440863 segs, 114992915 residues Searched:

440863

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Ggn2\_6/ptodata\_12/pubpaa\_VBS0\_NEW\_FUB.pep:\*
(cgn2\_6/ptodata\_12/pubpaa\_VBC\_NEW\_FUB.pep:\*
(cgn2\_6/ptodata\_12/pubpaa\_VBC\_NEW\_FUB.pep:\*
(cgn2\_6/ptodata\_12/pubpaa\_VBS0\_NEW\_FUB.pep:\*
(cgn2\_6/ptodata\_12/pubpaa\_VBS0\_PUBCOMB.pep:\*
(cgn2\_6/ptodata\_12/pubpaa\_VBS0\_PUBCOMB.pep:\*
(cgn2\_6/ptodata\_12/pubpaa\_VBS0\_NEW\_FUB.pep:\*
(cgn2\_6/ptodata\_12/pubpaa\_VBS0\_NEW\_FUB.pep:\* Published\_Applications\_AA:\* 11: 12: 13: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## STIMMARTES

Segmence 1117. An	1118	Sequence 1119, Ap	942, 7	Sequence 943, App	810.	510.	642,	Sequence 809, App	Sequence 2, Appli	Sequence 945, App	Sequence 16, Appl	Sequence 954, App	Sequence 2. Appli	Sequence 26, Appl	12		921	Sequence 807, App	Sequence 8, Appli	395,	8	18	77.	923	Sequence 7, Appli
OS-09-754-853A-1117	US-09-7	US-09-754-853A-1119			) US-10-101-464A-810	P US-10-101-464A-510	NS-10-101-464A-642	F US-10-101-464A-809	. US-10-149-846-2	. US-10-101-464A-945	US-10-208-948-16	US-10-101-464A-954	US-09-823-394-2	.0 US-09-862-027-26	9 US-1C-101-464A-915	US-10-101-464A-78	US-10-101-464A-921	US-10-101-464A-807	.0 US-09-838-955-8	US-10-101-464A-895	US-10-101-4643-58	US-08-910-386A-18	US-10-101-464A-77	US-10-101-464A-923	.0 US-09-838-955-7
894		894 9			717 9	365 9	919 9	1133 9	794 9	502 9	901 9	1021 9	1196 9				974 9	1014 9	339 1	6 866	999	960 8	632 9	823 9	286 1
18.6	18.6	18.6	18.6	18.4	18.4	18.1	18.1	18.1	17.9	17.7	17.5	17.5	17.5	17.4	17.4	17.2	17.0	15.8	16.6	16.5	16.4	16.4	16.2	16.2	16.2
641.5	641.5	641.5	641	636.5	635	626.5	624	624	613	612.5	603	604.5	604.5	601	109	593	587.5	580.5	574	568.5	566.5	565	560.5	559	558
20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	32	36	37	38	39	40	; -1 •#	42	Θ <b>Τ</b>	7	5

## ALIGNMENTS

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61 PSPPTPSTPGSPPELPQPSPPAPTTPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRP 120
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              Sequence 2, Application US/10086464

Publication No. US20020199218A1
GENERAL INFORMATION:
TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REPERENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464

PRIOR APPLICATION NUMBER: US 10/069,304

PRIOR APPLICATION NUMBER: ECT/CA0/00966

PRIOR FILING DATE: 2002-02-19

PRIOR APPLICATION NUMBER: ECT/CA0/00966

PRIOR PLING DATE: 1999-08-19

PRIOR PLING DATE: 1999-10-13

PRIOR PLING DATE: 1999-10-13

SOFTWARE: PRECEDING DATE: 1999-10-13

SOFTWARE: PRECEDING OFFICE TOWN NUMBER: US 60/159,122

SOFTWARE: PACENTING DATE: 1999-10-13

SOFTWARE: PACENTING DATE: 1999-10-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 3453; DB 9; Length 647; 100.0%; Pred. No. 9.1e-143; Live 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 647; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRF; ORGANISM: Brassica napus
US-10-086-464-2
US-10-086-464-2
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                                                      YSDRPVLPPPSPGLYLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGYLPSGKEV
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| Publication No. US2020199218A1
| CENERAL INFORMATION:
| APPLICANT: GORING, Dapine R. et al.
| TITLE OF INVENTION: PROLINE-RICH EXTERSIN-LIKE RECEPTOR KINASES
| FILE REFERENCE: P. 25,762-A. 08A
| CURRENT APPLICATION NUMBER: US/A
| CURRENT FILING DATE: 2002-02-28
| PRIOR FILING DATE: 2002-02-19
| PRIOR FILING DATE: 2000-02-19
| PRIOR FILING DATE: 2000-08-18
| PRIOR APPLICATION NUMBER: US 60/149,466
| PRIOR FILING DATE: 1999-08-19
| PRIOR FILING DATE: 1999-08-19
| PRIOR FILING DATE: 1999-08-19
| PRIOR FILING DATE: 1999-10-13
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100.0%; Pred. No. 1e-142;
ive 0; Mismatches 0;
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Les 647; Conservative
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LENGIH: 721
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APPLICALNT: GORING, Daphne R. et al.

TITLE OF INFORMATION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

FILE OF INFORMATION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

CURRENT APPLICATION NUMBER: US/10/086,464

CURRENT FILING DATE: 2002-02-18

PRIOR RELIGNED AND ENER: US 10/069,304

PRIOR RELIGNED AND ENER: US 10/069,304

PRIOR PLICATION NUMBER: US 60/0866

PRIOR FILING DATE: 2000-08-19

PRIOR PPLICATION NUMBER: US 60/149,466

PRIOR PPLICATION NUMBER: US 60/149,466

PRIOR PLING DATE: 1999-08-19

PRIOR PLING DATE: 1999-08-19

PRIOR PLING DATE: 1999-10-13

SOFTWARE: PACHALING DATE: 1999-10-13

SOFTWARE: PACHALING DATE: 1999-10-13

SOFTWARE: PACHALING VET. 2.1
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Pred. No. 9.1e-143;
0; Mismatches 0;
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Publication No. US20020199218A1
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US-10-086-464-4
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Best Local S:
Matches 647;
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Publication No. US20020199218A1

GENERAL INFORMATION:

APPLICAMTS GORING, Daphne R. et al.

TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES

TITLE OF INVENTION: DAPR: US/069,464

CURRENT APPLICATION NUMBER: US/10/086,464

PRIOR APPLICATION NUMBER: US 10/069,304

PRIOR PILING DATE: 2002-02-19

PRIOR PILING DATE: 2000-08-18

PRIOR PILING DATE: US 60/159,122

PRIOR PILING DATE: 1999-08-19

PRIOR PILING DATE: 1999-10-13

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity 51.8%.
Matches 368; Conservative
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US-10-086-464-14
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511 YVDDSLVDMARPLLINRASEQGDFEGLADAKMNNGTDREEMARMVACAAACVRBSARRRPR
PSSPSPSSPSSDGLSTGVTVGIAIGGVALLVIVTLICLLCKKKRRRDEEDAYYVPPPPPP
                 GPKAGGPTGGQQQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPFMSSSGGSD
                                                                                YSDRPVLPPPSFGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEV
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TILL OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILE REPERSENCE: P 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-28
PRIOR PRIOR APPLICATION NUMBER: US 10/069,304
PRIOR PLING DATE: 2002-02-19
PRIOR PLING DATE: 2000-08-18
PRIOR PLING DATE: 2000-08-18
PRIOR PLING DATE: 1999-10-13
PRIOR PLING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
SPRIOR FILING DATE: 1999-10-13
SOFTWARE: PARENTING DATE: 1999-10-13
SOFTWARE: PARENTING PARE: 2.1
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Matches 363; Conservative
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    ---PTRN 99
                                                                                                                                 192 QQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPPMSSSGGSDYSDRPVLPPPS
                                                                                                                                                                          YVDDSLVDWARPLINRASEQGDFEGLADAKMNGYDREEMARMVACAAACVRHSARRPR
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| Publication No. US20020199218A1
| GENERAL INFORMATION:
| APPLICANT: GORING, Daphne R. et al.
| TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
| FILE REPERENCE: P. 25, 762-A USA
| CURRENT APPLICATION NUMBER: US. 10,086, 464
| PRIOR APPLICATION NUMBER: US. 10,069, 304
| PRIOR PAPLICATION NUMBER: US. 10,069, 304
| PRIOR PAPLICATION NUMBER: PCT/CA00/00966
| PRIOR PILING DATE: 2000-08-18
| PRIOR PILING DATE: 1999-08-19
| PRIOR PILING DATE: 1999-08-19
| PRIOR PILING DATE: 1999-10-13
| NUMBER OF SEQ ID NOS: 27
| SOFTHARE: PATENTIN UND NOS: 27
| SOFTHARE: PATENTIN UNS: 21
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Pred. No. 2e-54;
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                                            100 PPP----
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LENGTH: 731
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                                                         ----APPPTTPSSPPP
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                                                                                                                                                                                                                                                                                                                                          --PPPGPKAGGPYGGQQQQWRQQNATP
                                                                                                                                                                                                                                                                                                                                                                            268 RRKKKR--NIDSYNHSQYLPHPNFSVKSDGFLYGQDPGKGYSSGPNGSMYNNSQQQQSSM
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 Gaps
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TITLE OF INVENTION: PROLINE-RICH EXTENSIN-LIKE RECEPTOR KINASES
FILLE REFERENCE: P. 25,762-A USA
CURRENT APPLICATION NUMBER: US/10/086,464
CURRENT FILING DATE: 2002-02-38
PRIOR APPLICATION NUMBER: PCT/CA00/00966
PRIOR PILING DATE: 2000-02-19
PRIOR PILING DATE: 2000-08-18
PRIOR PLING DATE: 1000-08-18
PRIOR FILING DATE: 1099-08-15
PRIOR FILING DATE: 1099-08-15
PRIOR FILING DATE: 1099-10-13
PRIOR FILING DATE: 1999-10-13
169;
Indels
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Mismatches 156;
                                 2 SSAPSPGTGSPPSPSNSTTT-----TPPPAS-
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CURRENT FILING DATE: 2002-03-18
PRIOR APPLICATION NUMBER: 09/704,302
PRIOR FILING DATE: 2000-11-01
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-12
PRIOR FILING DATE: 1999-01-10
PRIOR FILING DATE: 1999-01-01
PRIOR FILING DATE: 1999-01-01
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 989
SEQ ID NO 76
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Publication No. US20030046728A1
                                                                                                                                                                                                                               ORGANISM: Eucalyptus grandis
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Sequence 76, Application No. US2030046728A1

Fublication No. US2030046728A1

Fublication No. US2030046728A1

Fublication No. US2030046728A1

Fublican: Applican: Strabala, Timothy

APPLICANT: Higgins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000.1020c2

CURRENT APPLICATION NUMBER: US/12/101,464A
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                                                                                                                                                                                                                                                                                                                                            224 PFFGPAGQLPDGTVAPPIGPVIEPKISPAESISPGTPQPLVPKSLPVTTSTHRSSAGFLF
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                                                                                                                                                                  Gaps
                                                                                                                             Query Match
40.5%; Score 1399; DB 9; Length 731;
Best Local Similarity 47.3%; Pred. No. 1e-53;
Matches 317; Conservative 71; Mismatches 181; Indels 101;
                                                                              CRGANISM: Arabidopsis thaliana
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718 NPSQSSSEHQ 727
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NUMBER OF SEQ. ID NOS: 27
SOFTWARE: Patentin Ver.
SEQ ID NO 17
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US-10-101-464A-76
                                                                                   ) CRGANISM: AI
US-10-086-464-17
                                                  LENGIH: 731
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GENERAL INFORMATION:

APPLICANT: Strabala, Timothy
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Thair Use in the Modification of Plant Cell Signaling
FILE REFERENCE: 11000.1020-2
CURRENT APPLICATION NUMBER: US/10/101.464A
PRIOR RILING DATE: 2002-03-18
PRIOR FILING DATE: 2002-01-101
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                                                                                                                                                                                                                                                                                         285
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                                                                                               118 PRPPSSP----SP---PSPSSDGLSTGVVVGIAIGGVALLVIVILICLICKKKRRDEE 169
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                                                                                                                                                                                                                                                                                                                                                                                      286 FGYVHKGYLPSGKEYAVKQLKVGSGQGEREFQAETISRVHHRHLVSLVGYCIAGAKRL
                                                                                                                                                                                                                                                                                      PPPPPPPPMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGG
     Length 968;
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; ORGANISM: Physcomitrella patens
US-09-828-313-27
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Patent No. US2002050562A1

GENERAL INFORMATION:
PAPLICANT: COSTA e SILVA, OSWALDO DA
APPLICANT: HILLEAN NOCHA VAN
APPLICANT: THIELEN, NOCHA VAN
APPLICANT: CHEN, ROUTING
APPLICANT: GHEN, ROUTING
APPLICANT: SARRIA-MILLAN, ROBRIGO
TITLE OF INVENTION: USE IN PLANTS
FILE REFERENCE: 16113-0032
CURRENT APPLICATION NUMBER: US/09/828,313
CURRENT APPLICATION NUMBER: 00/196,001
PRIOR FILING DATE: 2000-04-07

NUMBER OF SEQ. ID NOS: 128

FORMINAND: DEALLY VOL.
                                                                                                                                                                                                                                                                                                               90 PAPVIPPIRNPPPSVPGPP---SNPSREGGSPRPPSSPSPPSPSSDGLSTGVVVGIAIGG 146
                                                                                                                                                                                                                                                                                                                                                                                    147 VALLVIVILICLICKKKRRRDEEDAYYVPPPPPGPKAGGPYGGQQQQWRQQNATPPSDH 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                     287 VVTSLPPPPRAPSPPRQPPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYE 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          267 ELARATNGFSEANLLGQGGFGYVHKGYLPSGKEVAVKQLK-VGSGQGEREFQAEVEIISR 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKIASDTNTHVSTRVMGTFGYLA 443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---------FEDVPA--EEDPEVHLGQLK-RFSLR 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PEYAASGKLIEKSDVFSFGVVLLELITGRRPVJANNTYVDDS--LVDWARPLLNRASEQG 501
                                                                                                                                                                                                                                                                                                                                      252 AALLF-----WRRRK---POEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21.3%; Score 735; DB 9; Length 630; 37.2%; Pred. No. 4.8e-25;
                                                                                                                                                                                                                                                                                68; Mismatches 125;
FRICR APPLICATION NUMBER: 09/228,986
PRIOR FILING DATE: 1999-01-12
PRIOR PILING DATE: 1999-11-01
PRIOR PILING DATE: 1999-11-01
PRIOR PILING DATE: 2000-01-11
PRIOR FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 969
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 37.28
Matches 175; Conservative
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                                                                                                                                                                                            ORGANISM: Pinus radiata
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SEQ ID NO 27
LENGTH: 749
TYPE: PRT
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RESCULT 11

US-10-101-464A-927

Sequence 927, Application US/10101464A

Publication No. US2003-046728A1

GENERAL INFORMATION:
APPLICANT: Strabala, Timothy
APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Strabala, Timothy

APPLICANT: Higgins, Colleen W.

ITILE OF INVENTION: and Their Ose in the Modification of Plant Cells

ITILE OF INVENTION: and Their Ose in the Modification of Plant Cell Signaling

FILE REPERBUCE: 11000-1020-2

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2000-11-01

PRIOR FILING DATE: 2000-11-01

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-01

PRIOR APPLICATION NUMBER: 60/162,866

PRIOR PLING DATE: 2000-01-11

WUMBER OF SEQ ID NOS: 989

SOFTHARE: FastSEQ for Windows Version 4.0
                                                                                                    158
                                                                                                                               ----YGGQQQQWRQQN 199
                                                                                                                                                                                                                                                311 CCRKRSKKALGDPEATTSSRRPWFTPPLSAKSOSDPSKSJDKTTKRNIFGSSKSEKKS-- 368
                                                                                                                                                                                                                                                                                                                                                                                                       253 GLVLGFSKST-----FTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGKE 299
                                                                                                                                                                                                                                                                                                                                                                                                                                       300 VAVKQLKVGSG--QGEREFQAEVELISRVHHRHEVSLVGYCIAGAKRLLVYEFVPNNNLE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              358 --LHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKV 415
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                                                    Gaps
                                               84;
Length 749;
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                     ---SKHRVFEPAPLDKGAADEPVVKASPPVKVLKAPPSFKGIS--
                                            76; Mismatches 160;
                                                                                                                                                                                                 159 LCKKKRRR---DEEDAYYVPPP---PPPGPKAGGP----
20.9%; Score 722; DB 10; 35.6%; Pred. No. 2.3e-24;
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QPEPEFRPPMSEVVQAL 719
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                       Best Local Similarity 35.6%
Matches 177; Conservative
                  Similarity
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Query Match
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RESULT 13
US-10-101-464A-74
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Publication No. US20030046728A1

GENERAL INFORMATION:

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Strabala, Timothy

APPLICANT: Nieuwenhuizen, Nicolaas

APPLICANT: Highins, Colleen M.

TITLE OF INVENTION: Compositions Isolated from Plant Cells

TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling

FILE REFERENCE: 11000,102062

CURRENT APPLICATION NUMBER: US/10/101,464A

CURRENT FILING DATE: 2002-03-18

PRIOR APPLICATION NUMBER: 09/704,302

PRIOR FILING DATE: 1999-01-12

PRIOR PELING DATE: 1999-01-12

PRIOR PLING DATE: 1999-11-01

PRIOR PLING DATE: 1999-01-01

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12

PRIOR PLING DATE: 1999-01-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 TIPGSPPAPVIPPIRNPPSVPGPPSNPSREGGSPRPPSSPS--PPSPSSDG-----L 134
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                                                                                                                                                                                                                                                                                                                                                                            263 FIYEELARAINGESEANLLGQGGFGYVHKGYLPSGKEVAVKQLK----VGSGQGEREFQA
                                                                           319 EVELISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIAL
                                                                                                                                   439 FGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVD----ANNVYVDDSLVDWARPLL
                                                                                                                                                                                                                                                                                                               495 NRASEQGDFEGLADAKMNNGYDREEMARWYACAAACVRHSARRPRMSQIVRALEGNVSL
                                Gaps
                              47;
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                                Indels
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                              92;
   DB 9;
Score 704.5; DB 9
Pred. No. 1.1e-23;
                             71; Mismatches
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 80
LENGTH: 707
 20.4%;
                              Matches 151; Conservative
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Best Local Similarity 34.0
Matches 178; Conservative
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US-10-101-464A-80
                 Similarity
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 Query Match
Best Local
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APPLICANT: Misuwenhaizen, Nicolaas
APPLICANT: Higgins, Colleen M.
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
FILE REPERENCE: 11060.1020c2
CURRENT APPLICATION NUMBER: US/10/101,464A
CURRENT FILING DATE: 2002-03-18
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/728,986
PRIOR PILING DATE: 1999-01-12
PRIOR APPLICATION NUMBER: 06/122,866
PRIOR FILING DATE: 1999-11-01
PRIOR APPLICATION NUMBER: 07/162,866
PRIOR FILING DATE: 1999-11-01
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                                                                                                                                                                     441
                                                                                                                                                                                                                               308 G--SGQGEREFQAEVEIISRVHHRHLWSLVGYCIAGAKRLLVYEFWFWNNL--ELHLHGE 363
                                                                                                                                                                                                                                                                                       501
                                                                                                                                                                                                                                                                                                                                                 364 GRPIMERSTRLKIALGSAKGLSTLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKI 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  424 ASDINIHVSTRVMGTFGYLAPETAASGKLITEKSDVFSFGVVLLELITGRRPVDANNVYVD 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      195 WRQQNATP--PSDHVVTSLPPPRAPSPPRQPPPPPPPPPPFMSSSG-----GSDYSDRPVL 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          371 STRLKIALGSAKGLSYLHEDCNPKJIHRDIKASNILIDFKFEAKVADFGLAKIASDTNTH 430
                                                                                                                                                                                                                                                                 442 STLSIQRPEDFLDAVSNISRLHHPRITELVGYCTEHEQYLLVYEYFDNGSLYDVLHMADE
                                 330 SNRVSFTPLSPLDAELLKESPEQKYSSSPLEIALKPPPSERNKSTGDKGFGSIFSSKRTK
                                                                                                              248 PPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLFSGKEVAVKQLKV
                                                                                                                                             484 DSLVDKARPLLNRASEQGDFEGLA---DAKMNNGYDREEMARMVACAAACVRHSARRPR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      541 MSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQY 583
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live 68; Mismatches
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NUMBER OF SEQ ID NOS: 989
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 74, Application US/10101464A
Publication No. US200300465728A1
SERMERAL INFORMATION:
APPLICANT: Strabala, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 43.1%
Matches 147; Conservative
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ch completed: July 2, 2003, 15:20:53 time : 37 secs
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US-10-219-220-263
           RESULT 15
US-10-219-220-263
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Job tim
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APPLICANT: Nieuwenhuizen, Nicolaas
APPLICANT: Higgins, Colleen M.
TITLE OF INVENTION: Compositions Isolated from Plant Cells
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: and Their Use in the Modification of Plant Cell Signaling
TITLE OF INVENTION: 0002-03-18
PRIOR PLICATION NUMBER: 09/704,302
PRIOR PLICATION NUMBER: 09/728,986
PRIOR PLICATION NUMBER: 09/228,986
PRIOR PLICATION NUMBER: 00/162,866
PRIOR PLICATION NUMBER: 00/162,866
PRIOR PLICATION NUMBER: PCT/USOU/00724
PRIOR PLICATION NUMBER: PCT/USOU/00724
PRIOR PLICATION NUMBER: PCT/USOU/00724
PRIOR PLICATION NUMBER: PCT/USOU/00724
                                                                        VSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGYTLELITGRRPVD----ANNVYVDDSL 486
                                                                                                       VDWARPLINRASEQGDFEGLADAKMNNGYDREEMARWYACAAACVRHSARRPENSQIVR 546
                                                                                                                                                                                                                                                                               LDWYKKL----BGEKKLHLLADKDLKGNFDRVELEEMVQVSLLCTQFQPGHRPFKMCDVLR 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 FTYEELARATNGFSEANLLGQGGFGTVHKGVLPSGKEVAVKQLK-VGSGQGEREFQAEVE 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 IISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :|| ||:|: | ||:|| :|| ||:|| 350 MISLAVHRNLLRLFGECHTQTERLLVYPYMSNGSVATEL--RAKPTLEWSTRKRIALGAA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVADFGLAKIASDTNTHVSTRVMGTFGY 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAPEYAASGKLIEKSDVFSFGVVLLELITGRRPVD----ANNVYVDDSLVDWARPLLNRA 497
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   PTRKRIALGAARGLLYLHEQCDPKIIHRDVKAANILLDEYFEAVVGDFGLAKLLDHRDSH 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 NEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKKERKMALGTQEYNATGEYSNPTSDYGL 615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                    547 ALEGNVSLSDLNECMRPGQSNVYS----SYGGSTDYDSS 581
                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 989
SCFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 812, Application US/10101464A
Publication No. US20030046728A1
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GENERAL INFORMATION:
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US-10-101-464A-812
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US-10-101-464A-812
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APPLICANT: Flinh, Barry
APPLICANT: Lasham, Annette
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Compositions affecting programmed cell
TITLE OF INVENTION: Cadath and their use in the modification of plant development
FILE REFERENCE: 11000.1022c1
CURRENT PEPLICATION NUMBER: US/10/219,220
CURRENT FILING DATE: 2002-08-14
PRIOR PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 290
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 263
LENGTH: 366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 GVLPSGKEVAVKQLKVGS-GQGEREFGAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              351 VPNNNLELHLHG------EGRPTNEWSTRLKIALGSAKGLSYLHEDCNPKITHRDIKAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         404 NILIDFKFEAKVADFGLAKIASDINTHY-STRVMGTFGYLAPBYAASGKLTEKSDVFSFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463 VVLLELITGRRPYDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 366;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         19.1%; Score 661; DB 9; L
43.1%; Pred. No. 5.2e-22;
live 57; Mismatches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               523 MVACAAACVRHSARRRPRMSQIVRALE 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 263, Application US/10219220
Publication No. US2003G082724A1
GENERAL INFORMATION:
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Matches 141; Conservative
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

2, 2003, 15:20:18; Search time 53 Seconds (without alignments) 1173.565 Million cell updates/sec July Run on:

Title: Perfect score: Sequence:

US-10-086-464-2 3453 1 MSSAPSPGTGSPPSPSNST.....REMENGKIKRTGQGYSGPSL 647

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000500000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR\_73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. Wo. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	probable protein k	hypothetical prote		hypothetical prote					·	protein F20B24.6 [	hypothetical prote	protein kinase hom	probable serine/th				probable serine/th	hypothetical prote	protein kinase hom	probable protein *	hypothetical prote	probable protein k	probable receptor	hypothetical prote	probable receptor-	hypothetical profe		hypothetical prote	69.4K hypothetical	
SUMMAKIES		£84564	A96529	T05264	D96728	D96711	F86387	B86369	104455	A96563	GB6239	C96728	T01477	T01502	E84587	G96593	T01086	T01711	A86146	T05994	B96609	E96602	D84860	G96602	G86227	G84510	H96740	T47793	F96602	D86466	
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	д	633	669	674	710	7.08	760	731	731	509	715	394	321	767	435	676	492	450	497	523	495	828	464	2062	482	520	109	512	1029	628	
dф	Query Match			æ.		42.3	41.5	41.0	40.5	40.5	35.7	29.6	28.2	23.6	23.2	22.4	22.4	22.3	22.1	21.9	21.7	21.6	21.6		21.2		21.0		20.8	20.8	
	Score	1748.5	1729	1687	1515.5	1459.5	1434	1415.5	1399	1397	1233	1022	973	816.5	802	774	773	769.5	764	757	749.5	745	744.5	Ω <sub>+</sub>	732.5	26	24	22	719	717	
	Result No.	г	Cŧ	æ	<del>-1</del>	ស	9	7	o	on ·	10	11	12	13	14	15		17	18	19	20	21	22	23	24	25	56	27	28	29	

serine/threonine-s	probable somatic e	hypothetical prote	probable serine/th	protein kinase-lik	hypothetical prote	probable serine/th	protein serine/thr	hypothetical prote	probable Serine/Th	hypothetical prote	hypothetical prote	protein F12M16.30	probable protein k	probable LRE recep	serine/threonine.s
52	54	91	48	01	74	70	17	74	33	4.5	14	74	86	30	85
T491	T14354	C962	T008	T483	C962	T052	TS0817	D96574	E36633	D8624	386214	A96574	<b>G84686</b>	684630	T52285
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## ALIGNMENTS

339 IAGAKRILIVYEEVPNNNLELHIHGEGRPIMEWSTRIKIALGSAKGISYLHEDCNPKIIHR 398

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9 6	OV 299 EVAVKOLKVGSGOGRRREDARVETTGRVHHBUTVGT VGVCT - AGAMBIT 1990BDNNNH B. 267
OY SAY DIAKASHILDERKEBAYADEGGAKIASDINTHYSIRYNGIFGYIAPBYAASGKLIEKSDY 458 	360 EIAVKSLKAGSGQGEREFQAEVEIISRVHHRHIVSLVGYCSNAGGQRLLYYEFIPNDILE
	QY 358 LHLHGEGRPTMEMSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFRFRAKVAD 417
50 DUNDARIA CARACTERISTICA CARACTERISTICA CONTRACTOR CO	
	480 FGLAKLSQDNNTHVSTRVMGTFGTLAPEYASSGKLTEKSDVFSFGVMLLELITGRGPVDL
OY 579 DSSQYNEDDMKKFRKMALGTQEY NATGEYSNPTSDYG 614	QY 478 INVYVDDSLYDWARPLINRASEQGDFEGLADAKMNNGYDREEMARWYACAAACVRHSARR 537 : ::
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RESULT 2 A96529	
hypothetical protein F13F21.28 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear oress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text change 17-May-2002	QY 598 QEYNATGEYSDYGLYPSGSSSEGOTTREMEMGKIKRTGQG 641
nite, O., Alon	
r.r.; Lewar,	
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Lil, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial Rizzo, M. Doonew m	ਹਾਜ਼
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R w	C;Accession: T05264 R;Bevan, M.; Terryn, W.; Ardiles, W.; Buysshaert, C.; Dasseville,
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A:Reference number: A86141; MUID:21016719; PMID:11130712	ewes, n.w.; mayer, K.F.X.; Schueller, C. submitted to the Protein Sequence Database, September 1998 A.Reference number: 215406
A; Accessor: Asorz A; Status: preliminary A; Molecule type: DNA	A; Accession: T05264 A; Molecule type: DNA
A;Residues: 1-699 <sio> A;Cross_references: GB:AE005173; NID:g5430769; PIDM:AAD43169.1; GSPDB:GN00141</sio>	A; Kesidues: 1-6/4 (2EV) A; Cross-references: EMBL: A1023094 A; Experimental source: cultivar Columbia: BaC Alone miton
	C;Genetics: A;Map position: 4 A;Introns: 180/1; 221/1; 381/1: 421/1: 444/3: 470/2: 518/3: 583/3
unassigned	A,Note: 14L20.20 C,Superifanily: assigned Ser/Thr or Tyr-specific protein kinas
	Onorg Watch
CAPONS TITTPPPASAPPPTESSPPPESTIPISPPP	<pre>vuely match vuely match Vuely match Best Local Similarity 51.8% pred, No. 3.3e-47; Matches 368; Conservative 87; Mismatches 140; Tridels 114. Game 25.</pre>
Db 9 NSPRAPPPSSPPSSPNDQTTSPPRSDNQETTSPPRPSSPDIAPPRQQQGESPPPLP 68	1 MSSAPSPGIGSPPSPSNSTIITPPPASAPPTTPSSPPPSTIPTSPPPSSRSTPSAPP 6
6.9 E	QY 61 PSPPTPSTPGSPPPLPQPQ-PA-PUTPGSPPA-PVTPPTRM 99
QY 8/ GSPPAPYTPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSPSPSSDGLSTGVVQIAIGG 146	Db 59 PAPPIQETSPETSPSSSPPVVANPSFQTPENPSPPAPEGSTPVTPPAPPQTPSNQSPERP 118
	OY 100 PPPSVPGPPSNPSREGGSPRPPSSPSPSSSDGLST 136  Db 114 TPPSDSZNINDRUFNCANNINDROGENERSPACEMENT 136  TO TPPSDSZNINDRUFNCANNINDROGENERSPACEMENT 136  TO TPPSDSZNINDRUFNCANNINDROGENERSPACEMENT 136  TO TPPSDSZNINDRUFNCANNINDROGENERSPACEMENT 136  TO TPPSDSZNINDROGENERSPACEMENT 136  TO TPSDSZNINDROGENERSPACEMENT 13
	137 GVVVGIALGGVALLVIVTLICLICKKKRRDBEDAYVVPPPPPPPGFA-GGPYGGO
244 NDHIV-NLPPPPGSMGTNWWSSPPPPPPPGNWQPMPSPPAPVSGGANVIQSGEMS	PPPFMSSSGGSDYSDRPV
OY 242 SDRPVLPPPSPGLVLGFSKSTFITEELARATNGFSEANLLGGGGFGTVHKGVLPSGK 298    Do	229TPQDHVV-NMAGQGGGNWGPQQPVSGPHSDASNLTGRTAIPSPQ
า	VY 252 PGLVLGFSKSTFTYEELARATNGFSFANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQ 311

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Page 3

q		Qy 163 KRRKDEEJAYYVPPPPPGPKAGGPYGGOOOWROONATPPSDH 206
δ 1	GEREPQAEVELISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWS	:  :  :
S S		QY 207 VVISLPPPPKAPSEPRQPPPPPPPPPSPGSGSSGSDKDRPVLPPPSPGLVLGFSKSTFTYE 266
Å da	372 TRLKIALGSAKGLSYLHEDCNPXIIHRDIKASNILLIDFKFEAKVADFGL 420	SSGQŤH DAEVEL
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q <sub>Q</sub>		OY 327 HHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLKGEGRPTMEWSTRLKIALGSAKGLSY 386
op oð	481 YVDDSLVDWARFICKRASEQGPFEGLADAKMNNGYDREEMARNVACAAACVRESARRRPR 540 ::	Db 405 HHRHILVSLVGYCIADSERLLIYEYVPNQTLEHHLHGKGRPVLEWARRVRIAIGSAKGLAY 464 Ov 3R7 IHRHGVNDKTTHRDTXASVHTITDRKERAXVAADRGTAKTASDAWHHUSERDVMGYRGYLADRY 446
QY		465 LHEDCHFYIIHPINKSANILLDDEFFRAQVADFGLAKINDSTQTHVSTRVMGTFGYLAPER
QQ Q	570 MSQVQKLIPLVGSIIVRALEGDMSMDDLSEGIRPGQSTYLSPGSVSETDASSTADMKK 629	Qy 447 AASGKLTEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLNRASEGGDFEGL 506
<i>8</i> 8	FRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMGKIKRTGQ 64	Db 525 AQSGKLTDRSDVFSFGVVLLELITGRRPVDQYQPLGEESLVEWARPLLHKAIFTGDFSEL 584
DD PFSHTM A	630	QY 507 ADAKMNNGYDREEMARWACAAACWRHSARRRPRMSQIVRALEGNVSLSDLNEGMRPGQS 566   ::   :
D96728	cal protein F24313.3 [imported] - Arabidonsis thaliana	OY 567 NVYSSYGGSTDYDSSQYNEDMKKERKMALGTQEYNATGEYSNPTSDYGLYPSGSSSGQ1 626
C.Specie C.Date:	C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 02-Mar-2001 *sequence revision 02-Mar-2001 *t-ext change 21-War-2001	Db 645 SAYDSGQYNNDTMKFRKMARGFDDSSDSGMYSGDYSVQDSRKGSNGAS 692
C; Access	sion: D96728	Qy 627 T 527
Chin, C	Chin, C.R.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Andrew N.F.; Hughes, B.; Huizar, L.	Db 693 S 693
A; Author	108, 815-825, 2000 :s: Hunter, J.i.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khavkin, E.; Kim, C.	RESULT 5
C.A.; Li	Marziali,	D96711
A; Author ker, M.;	Tallon,	hypotherical protein F44J5.8 [imported] - Arabidopsis thalland C;Species: Arabidopsis thalland (mouse-ear craft) C;Date: 02-Mar-2001 #sequence revision 02-Mar-2001 #text chance 31-Mar-2001
A;Title: A;Refere		C; Accession: D96711 R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo
A; Access A; Status		Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hutzar, L.
A; Residu	4 570> GR-BEAG173- NTD-46176186, DTNW-AABAAGG 1. CORDE.CHGA111	Nature 408, 816-820, 2000 A:Authors: Bunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C;Geneti A;Gene:	Serimodolisti strugotiotici struspedenti, daribiduootet	C.A.; L., O.H.; L., I., L., A.; L., S., L., S., L., L., L., L., L., L., L., L., L., L
A; Map po	n: 1	<pre>ker, M.; Nu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.</pre>
Vuery match Best Local Matches 33	aton cal Similarity 46.2%; Score 1515.5; DB 2; Length 710; 333; Conservative Bl; Mismatches 158; Indels 149; Gaps 19;	A;Reference number: A86141; MUD:21016719; PMID:11130712 A;Accession: D96711 A;Status: preliminary
Qy	SSAPSP-GTGSPPSPSNSTTTTPPPASAPPPTTPSSPPPSTI 44	A;Molecule type: DNA A;Residues: 1-708 cSTO- A;Cross-references: GB:AE005173: NID: G5734709: PIDN: AAD49974.1: GSPDB:GN0G141
qq	SAAPPPIDSAPPRSPADSSPPPALPSLPSAVFSPPPTVSSPPPPLDSSPPPPDL 83	C;Genetics: A;Gene: F24J5.8
Oy Dp	45 PTSPPPSSRSTPSAPPPSPPTPSPPTPSTPGSP 72   1	A; Map position: 1 Oner Match 128. Commo 1450 E. np 9. Tomath 700.
Qy	-	Similarity 41.88; Pred. No. 5.5e-40; 7; Conservative 90; Mismatches 127; Indels
qq	142 PPEQIPPPASSPQGGFKKPKKHHPGPATSPPAPSAPATSPPAPPNAPPRNSSHALPPKST 201	QY 1 MSSAPSPGTGSPPSPPSNSTT-TIPPPASAP-PPTTPSSPPPPSTIPTSP 48
Oy	105 FGPPSNPSREGGSPRPPSSPSPSPSSDGLSTGVVVGIALGGVALLVIVTLLCLLCKK 162	ATPPPVTSPI
අි	202 AAGGPLTSPSRGVPSSGNSVPPPANSGGGYQGKTWAGFAIAGFAVIALMAVVFLVRRK 259	Qy 49 PPSSRSTPSAPPPSPPTPSTPGSPPPLPQPSPPAPTTP 86

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Southwick, A.M.; Sun, H.; Tallc
Bavis, R.W.
plant Arabidopsis.
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Luros, J.S.; Maiti, R.; Marzie
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                           20;
                                                  P----PITPSSP-PPPSTIPT 46
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ERPSPPPGGBPKRREQPPPG 235
                                                                                                                                                                      NATPPSDHVVTSLPPPFKAPS 219
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                         Indels 136; Gaps
Length 760;
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A; Molecule type: DNA
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A;Residues: 1-731 <STO>
A;Cross_references: GB:AE005172; NID:g4056437; PIDN:AAC98010.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
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                                                                                                      Length 731;
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; Pred. No. 1.4e-38;
93; Mismatches 156; :
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Accession: A96563
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Aloi Chin, C.K.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
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                                                                                                                                                                                                                                                                                 1 MSSAPSPGTGSPPS---PPSNSTTTPPPASAP----PPTTPSSPPPPSTIPTSPPPSSR
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                                                                                                                                                                                     40.5%; Score 1399; DB 2; Length 731;
47.3%; Pred. No. 4.5e-38;
Live 71; Mismatches 181; Indels 101;
A)Cross-references: EMBL:AL022537
A)Experimental source: cultivar Columbia; BAC clone P4D11
C)Genetics:
A)Map position: 4
A)Introns: 326/1; 476/1; 505/1; 528/3; 557/2; 606/3; 660/3
A)Note: F4D11.90
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 47.38 tes 317; Conservative
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protein F24J13.2 [imported] - Arabidopsis thaliana
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Best Local Similarity
Matches 289; Conserv
                                                                                                 A; Molecule type: DNA
A; Residues: 1-715 <STO>
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C.A.; Li, J.E.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome I of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-509 SINOA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hudghes, B.; Huizar, L. Bature 408, 816-820, 2000
A; Arthors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzlali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
                                                                                                                                                                                                                                                                                79 SPPAPTIPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSPPSPSDGLSTCV 138
                                                                                                                                                        GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                            139 VVGIAIGGV-ALLVIVTLICLLCKKKR---RRDEEDAYYVPPPPPPPPRGPKAGGPYGGQQQQ 194
                                                                                                                                                                                                                                                                                                                                                             WRQQNATPPSDHVVTSLPPPPRAPSPPRQPPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGL 254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --EIGQNLFTYEDLSKAISNFSNFNLLGGGGFGYVHRGVLVDGTLVAIKQLKSGSGQGER 182
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 VLGFSKSTFTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGER
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                                                                                                                                                  A;Cross-references: GB:AE005173; NID:g10645450; PIDN:AAG21566.1; C;Genetics:
A;Gene: F13x6.9
                                                                                                                                                                                                                               Length 509;
                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                       120;
                                                                                                                                                                                                                             Score 1397; DB 2;
Fred. No. 4e-38;
                                                                                                                                                                                                                                                       70; Mismatches
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52.5%;
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Best Local
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                                                                                                                                                             PIDN: AMFE7672.1; GSPDB:GN00141
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A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
A; Accession: G86239
A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----VVVGIAIGGVALLVIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 SSSPSPPSLSGSNNHSGGSNRHNANSNGDGGTSQQSNESNYTEKTVIGIGIAGVLVILEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 AGVFFVRRKQKKGSSSPRSNQYLPPANVSVNTEGFIHXRQKPGNGNSS---AQNSSPDTN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206 HVVISLPPPPKAPSPPRQPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFIY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EELARATNGFSEANLLGQGGEGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEIISR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------TLAPEYASSGKLTDRSDVFSFGVVLLELITGRKPVDTSQPLGEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKKFRKMA----LGTQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLVDWARPLINRASEQGDFEGLADAKMNNGYDREEMARWYACAAACVRHSARRRPRMSQI
                                                                                                                                                                                                                                                                                                  198;
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                 PPSPPTPSTP-GSPP---PLPQPSPPAP--------
                                                                                                                                                                                                                                                                                                Mismatches 163;
                                                                                                                                                                                                                                                           DB 2;
                                                                                                                                                                                                                                                         Score 1233; DB 2
Pred. No. 8.1e-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHG-
                                                                                                                                                   A;Cross-references: GB:AE005172; NID:g6573752;
C;Genetics:
A;Gene: F20B24.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 PGSPPAPVTPPTR-----NPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 PSSPSPSSSSBGLSTG-----
                                                                                                                                                                                                                                                                                                84;
                                                                                                                                                                                                                                                         35.78;
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m

Gaps

12;

homology

413

473

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probable serine/threonine-specific protein kinase (EC 2.7.1.-) T10M13.2 - Arabidopsi: probable serine/threonine-specific protein kinase (EC 2.7.1.-) T10M13.2 - Arabidopsi: C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: 19-Feb-1399 #sequence_revision 19-Feb-1399 #text_change 04-Mar-2000
C;Accession: T01502
R;Johnson, A.F.; de la Bastide, M.; Lodhi, M.; Hoffman, J.; Hasegawa, A.; Gnoj, L.; (Martienssen, R.; McCombie, W.
Martienssen, R.; McCombie, W.
A;Description: The sequence of the Arabidopsis thaliana T10M13 BAC.
A;Reference number: 214346
A;Recession: T01502
A;Accession: T01502
A;Acc
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A:Cross-references: EMBL:AF001308; NID:g2104523; PID:g3912917
A:Cross-references: EMBL:AF001308; NID:g2104523; PID:g3912917
A:Experimental source: cultivar Columbia
C:Genetics: A:Map position: 4S
A:Introns: 132/1; 256/1; 327/1; 451/1; 532/2; 581/3
A:Note: T10M13.2
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom C:Reywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                            242 SDRPVLPPPSPGL---VLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGK 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFSKPSMKRNAQSPGAGLADIAPAOSSNGVLPDALTQPPLSPSISNCCKSDMVLKRRSIG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDC----NPKIJHRDIKASNILIDFKFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             414 KVADFGLAKIASDTNTHVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLJELITGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        474 PVDANNVYVDDSLVDWARPLLINRASEQGDFEGLADAKMINGYDREEMARMVACAAACVRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GSPPSP---PSNSTITT--PPPASAPPTTPSSPPPPSTIPTSPPPSSRSTPSAPPPSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLPVSPILSPSTSPVITDLPLPAEFPRFHRKYFAPQQAEAPQHSPPYSRLVASDHPPTSS
                                                                                                                                        A;Map position: 1
A;Introns: 136/1; 166/1; 189/3; 215/2; 264/3
C;Superfamily: kinase-related transforming protein; protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 707;
                                                                                                                                                                                                                                                                                                    Length 321;
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                                                                                                                                                                                                                                                                                                28.2%; Score 973; DB 2; I
61.7%; Pred. No. 7.1e-25;
iive 45; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 61.78
Matches 192; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SGPKRPRWVQV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                  C;Genetics:
A;Gene: ATSP:F1707.1
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Best Local 9
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C;Accession: 026728
R;Theologis, A; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Coway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.B.; Maria, C.A.; Liu, J.H.; Li, Y.; Lin, X.; Liu, S.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shino, P.; Southwick, A.M.; Sun, H.; Tallon, A;Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C56728
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-394 <SIO>
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C,Species: Argenta; V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, Y.Y. Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N. Submitted to the EMBL Data Library, June 1998
A; Description: Arabidopsis thaliana chromosome 1 BAC F1707 sequence.
A; Reference number: 214334
A; Accession: TO1477
A; Ascession: TO1477
A; As
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4.
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A)Gene: F24J13.2
A;Map position: 1
C;Superfamily: kinase-related transforming protein; protein kinase homology
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QVADFGLAKVNDTTQTHVSTRVMGTFGYLAPEYAQSGQLTDRSDVFSFGVVLLELITGRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             242 SDRPVLPPPSPGL---VLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.6%; Score 1022; DB 2; 57.0%; Pred. No. 2.4e-26; ive 54; Mismatches B2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match 29.6%
Best Local Similarity 57.0%
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              594 ALG 596
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alochin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzi, Rizzo, M.; Romey, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Talli, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Ritle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A80141; MuID:21016719; PMID:11130712
                              413
                                                                                                                                      414 KVADFGLAKIASDINTHVSTRVMGTFGXLAPEYAASGKLTEKSDVFSFGVVLLELITGRR 473
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           294 LPSGKEVAVKQLKVGSGQGEREFQAEVELISRVHHRHLVSLVGYCIAGAKRLLVYEFVPN 353
                                                                                             584
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C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   402
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                                                                                                                                                                                                                                                                                                                                                                                                                                              probable protein kinase, 86372-89112 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: G96593
                                                                                                                                                           19 EVSHRPFWGEVVQALK--LIYNDADETCGDYCSQKDSSVPDSADFKGDLAPSDSSSWMNLT
                                                                           NNLELHLHGEGRPTMEWSTELKLALGSAKGLSYLHEDCNPKIJHRDIKASNILIDFKFEA
                                                                                                                                                                                                     474 PVDANNVYVDDSLVDWARPLLNRASEQGDFEGLADAKMNNGYDREEMARMVACAAACVRH
                                                                                                                                                                                                                                                                     SARRRPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDY~~----DSSQYN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248 PPPSPGL------VLGFSKSTFTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPMNNLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     403 IVAVKQHKVASTQGDVEFCSEVEVLSCAQHRNVVMLIGFCIEDTRRLLVYEYICNGSLDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HIHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPK-IIHRDIKASNILIDFKFEAKVAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FGLAKIASDINTHVSTRVMGTFGYLAPEYAASGKLTEKSDVFSFGVVLLELITGRRPVDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 22.4%; Score 774; DB 2; Length 678
Best Local Similarity 48.6%; Pred. No. 2.6e-18;
Matches 156; Conservative 57; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                       :: : : | | | : | | : | | : | | 351 PRLRYGQASSFITMDYS----SGPLEDMENRPHSASS 383
                                                                                                                                                                                                                                                                                                                                   EDMKKFRKMALGIQEYNATGEYSNPTSDYGLYPSGSSS 622
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A;Molecule type: DNA
A;Residues: 1-676 <STO>
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A; Map position: I
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CHCVYPIKLDILLLNVSETPSWNMFINEFATQLGLLPHQIELINFYVLSLSRMNISMDIT 206
                                                             207 PHSGISFSASQASAINSSLISHKIOFSPTLYGDYKLLNEWFERPAPSQAPLVASSPHKA 266
                                                                                             SSDGLSTG-------VVVGIAIGGVALLVIVTLECLICKKKRRRDEEDAYYVP 175
                                                                                                                                                           176 PPPPPGPKAGGPYGGQQQQWRQQNATPPSDHVVTSLPPPFKAPSPPRQPPPPPFMSS 235
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                                                                                                                                                                                                                                                                                                             467
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C;Superfamily: kinase-related transforming protein; protein kinase homology
                                                                                                                                                                                                  ---KAPDPHKEAVKPRNLD-AGS
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-ive 68; Mismatches 122; Indels
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FSSGPYSGLSAFDHENITRITVFSEDLHEGR 707
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Matches 182; Conservative
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583 YRPKGQQCLIEWARSLL---EEYAVEELVDPRLEKRYSETQVICMIHTASLCIRRDPHL 638

538 RPRASQIVRALEGNVSLSDLN 558 |/|||||::|||||:::::: 639 RPRASQVLRLLEGEMIANEIS 659

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Search completed: July 2, 2003, 15:25:21 Job time : 56 secs

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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

1. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

RAPBL, AN128699; AAK12965.1; ...

RINGEPRO: IPR000290; Ser_thr_EMinase.

RINGEPRO: IPR001290; Ser_thr_EMinase.

RINGEPRO: PR00129; TYL_PKINASE.

REINTS: PR01017; PRCHEMEXTENSN.

PRINTS: PR010109; TYRKINASE.

RODOM: PR00109; TYRKINASE.

RODOM: PR00109; TYRK: 1.

RAPRT: SM00129; TYRK: 1.

ROSITE: PS00101; PROTEIN KINASE_ATP; 1.

ROSITE: PS00101; PROTEIN KINASE_ATP; 1.

RROSITE: PS00101; PROTEIN KINASE_ATP; 1.

RROSITE: PS00108; RROSEN SETING-PROTEIN KINASE_ATP; 1.

RROSITE: PS00108; RROSEN SETING-ATP; 1.

RROSITE: PS00108; RROSEN SETING-ATP; 1.

RROSITE: PS00108; RROSEN SETING-ATP; 1.
                                                                                                                                                                                                                                                                                                                                                   Receptor profesh Kinase PERKI.

Brassica napus (Rape).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicace; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
Silva N.F., Goring D.R.;
"Characterization of a novel Brassica napus receptor protein kinase
          29ask4
29ayi5
                          098977
094398
0919c5
094317
096319
09fw38
                                                                                             09fh74
09fu38
08rww0
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09snf3
004245
09sk72
09lic9
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094kd9
023699
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022764
004601
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091mm7
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01-JUN-2001 (TrEMBirel. 17, Last sequence update)
01-MAR-2002 (TrEMBirel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 3453; DB 10;
Pred. No. 6.4e-216;
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         05ASK4
09AYI5
0943GE
091QC5
09AJI7
09CAL9
09FW38
064591
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Best Local Similarity
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1392.5
1222.5
1222.3
1215
1209.5
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09x196 arabidopsis
09x196 arabidopsis
065672 arabidopsis
091s95 arabidopsis
091s97 arabidopsis
091x50 arabidopsis
095x31 arabidopsis
095x31 arabidopsis
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1514.915 Million cell updates/sec
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                                                                                                          1 MSSAPSPGTGSPPSPSRST.....REMEMGKIKRTGQGTSGPSL
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094jz6
                                                        July 2, 2003, 15:19:04; Search time 88 Seconds
       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                     671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
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Q9LV48
Q94JZ6
Q8W0B8
Q9LK03
Q9ZNQ8
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065672
09LS95
09CAL8
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Gapop 10.0 , Gapext 0.5
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1: sp_archea:*
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3: sp_fungi:*
4: sp_human:*
5: sp_huvertebrate:*
7: sp_hnc:*
8: sp_organelle:*
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                                                                PSPPTPSTPGSPPPLPQPSPPAPTTPGSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRP
                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2002 (TrEMBLrel. 21, Last annotation update)
Protein kinase-like protein (AT3924550/M0824_8) (Hypothetical 69.3 kDa
                      MSSAPSPGTGSPPSPPSNSTTTPPPASAPPPTTPSSPPPPSTTPTTPTSPPSSRSTPSAPP
                                PSSPSPPSPSSDGLSTGVVVGIAIGGVALLVIVTLICLLCKKKRRRDEEDAYYVPPPPPP
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                                                                                                                                                      GPKAGGPYGGQQQFRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPFMSSSGGSD
                                                                                                                                                                                                 YSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEV
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    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kaneko I., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S., Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'Structural analysis of Arabidopsis thaliana chromosome 3.
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  Mismatches
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MEDLINE=20363099; PubMed=10907853;
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647; Conservative
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Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki T.,
Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Phan P.K., Quach H.L., Sakurai T.,
Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
Tamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
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                                                                SEQUENCE FROM N.A.

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,

Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,

Cheuk R., Chung M.K., Hayashizaki Y., Ishidad J., Kaniya A., Kawai J.,

Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,

Sakurai T., Satou M., Seki M., Shinn P., Tamada K., Shinozaki K.,

Ecker J., Theologis A., Davis R.W.;

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170 DAYYVPPPPPPGPKAGGPYGGQQQQWRQQNATPPSD-HVVTSLPPPRKAPSPPRQPPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MSSAPSPGT---GSPPSPSSPSNSTTTTPPPA--SAPPPTTPSSPPP-PSTIPTSPPPSSRS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai Kim C., Lin J., Liu S.X., Narusaka M., Pham P.X., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-- SIMILARIY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length
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                                                                                                                                                                                                                                                                                                                                                                                                         "Arabidopsis cDNA clones."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
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Hypochetical protein; ATP-binding; Kinase;
Serine/threonline-protein kinase; Transferase.
SEQUENCE 652 AA; 69271 MW; 35005EE29F88602F CRC64;
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87.0%; Pred. No. 2.1e-182;
ive 24; Mismatches 41;
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PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMEL: AY056788; AAL10479.1; -.
EMEL: AY093065; AAM13064.1; -.
InterPro; IPR000719; EML, pkinase.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002996; Ser_thr_pkinase.
InterPro; IPR004040; STY_pkinase.
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PRINTS; PRO0109; TYRKINASE.
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Matches 574; Conservative
                 3AC clones.";
7:217-221(2000)
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                                 61 PPSLPPPSPPGSLT---PPIPQPSPSAPITP-SPSPTTPSNPRSPPSPNQGPPNIPS-
                                                                                                                                  TPSAPPPSPPTPSTPGSPPPLPQPSPPAPTTPGSPPAPYTPPT-RNPPPSVPGPPSNPSR
                                                                                                            EGGSPRPPSS--PSPPSPSSDGLSTGVVVGIAIGGVALLVIVTLICLLCKKKRRR--DEE
                                                                                                                                                                                                                DAYYVPPPPPPPPRAGGPYGGQQQWRQQNATPPSD-HVVTSLPPPRAPSPPRQPPPPP
                                                                                                                                                                                                                                                                                                                       PPP-FMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFG
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
butative receptor protein kinase PERK1.
0452F10.5.
0ryza sativa (Rice).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae, Oryza.
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EMBL, AP003434; BAB78668.1; -.
Interpro; IPR00019; Buk.pkinase.
Interpro; IPR000847; HTB_LysR.
Interpro; IPR001847; HTB_LysR.
Interpro; IPR001847; YT_PKinase.
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PROSITE; PSOC107; PROTEIN_KINASE_ATP; UNKNOWN_1.
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Sasaki T., Matsumoto I., Yamamoto
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Probom; PD000001; Buk_pkinase; 1.
SMART; SM00226; S_TKC; 1.
SMART; SM00219; TyTKC; 1.
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                                                  SOUTHWICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Scouthwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Southwick A., Karlin-Neumann G., Banh J., Carninci P., Chen H., Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P. K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K., Scher J., Theologis A., Davis R.W.; Submitted (APR-2001) to the NBL/GenBank/DDBJ databases.

EMBL, AF370509; AAK43886.1; -.

EMBL; AF370509; EWL, Pkinase.

InterPro; IPR002129; Ser_thr_pkinase.
                                                                                                                                                                                                                                                                                              LITGRRPYDANNYYVDDSLYDWARPLLNRASEQGDFEGLADAKMNGYDREEMARMYACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKFRKMALGTQEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMGKIKRTGQGYSGPSL
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AAYYVPPPPPSGPKAGGPYGGQQQYKQQQNASRPSDNHVVTSL-PPPKPPSPPRKPPPPPP
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Prodom: PF000001; Buk_pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_AIP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_SI; UNKNOWN_1.
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86.8%; Pred. No. 2.8e-182;
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SEQUENCE 652 AA;
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STRAIN-COLUMBIA;
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                                                                                                                                                                                                                                                                                                                  LVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHED
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                                                                            Gaps
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=COLUMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                            55;
                                                       Length 597;
                                                                          Indels
                                3809FC29A222FEB0 CRC64;
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01-CCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                     DB 10;
                                                                  10;
119;
 PS50311; PROTEIN_KINASE_DOM; 1.
PS03108; PROTEIN_KINASE_ST; UNKNOWN_1.
                                                52.8%; Score 10.1...
60.4%; Pred. No. 4e-11
+ive 69; Mismatches
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ETEMEMGSLKKDG 585
                                                                Local Similarity 60.4
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                     Receptor; Kinase.
SEQUENCE 597 AP
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AT2G18470.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Core eudicots; Rosidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
               thaliana chromosome 3. II.
4,251,695 bp covered by ninety
Nakamura Y.;

"Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninet
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL: AP000382; BAB02941.1;
ENSP; P12931; 1FMK.
                                                                                                                                                                                                                                                                                                       ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                               20;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                         458 AA; 50101 MW; BD580109B7158940 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYNATGEYSNPISDYGLYPSGSSSEGQTIREMEMGKIKRIGQGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TrEMBLrel. 10, Created)
(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                Score 1769; DB lu;
Pred. No. 7e-107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Z
                                                                                                                                                                                                                                                                                                                                                                                                             Matches 351; Conservative 34; Mismatches
                                                                                                                                   InterPro: IPR000719; Buk_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR004040; STY_pkinase.
InterPro: PF00069; pkinase; 1
Probom; PP000001; Euk_pkinase; 1.
SMART: SM00221; STYKC; 1.
PROSITE; PS000107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS000117; PROTEIN_KINASE_DOM; 1.
PROSITE; PS000108; PROTEIN_KINASE_DOM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            633
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                                                                                                                                                                                                                                                                                                                                                                           51.2%;
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288 NILGOGGFGYVHKGVLPSGKEVAVKSLKAGSGQGEREFQAEVDIISRVHHRYLVSLVGYC 347
                                              339 IAGAKRILUYEFVPNNNLELHLAGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHR
                                                                      FSFGVVLLELITGRRPVDANNVVVDDSLVDWARPLLNRASEQGDFSGLADAKMNMGYDRE
                                                                                                                                                                                                                                                             2 SSAPSPGTGSPPSPSNS--TTTTPPPA----SAPPPTTPSSPPPPSTIPTSPPP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---TP
                                                                                                                                        DIKASNILIDFKFEAKVADFGLAKIASDINTHVSTRVMGTFGYLAPEYAASGKLTEKSDV
                                                                                                                                                                                                                                                                                                                             EMARMVACAAACVRHSARRPPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSTGGSTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID-3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Federspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Arajo R., Huizar L., Rowley D., Buehler E., Dunn P., Gonzalez A., Kremenetskaia I., Kim C., Lenz C., Li J., Liu S., Luros S., Schwartz J., Shinn P., Toriumi M., Vysotskaia V.S., Walker M., Yu G., Ecker J., Theologis A., Davis R.W.; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

-! SIMILARIT: BELOMGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL, AC007504; AAD43169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00107; PROTEIN KINASE ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tch 50.1%; Score 1729; DB 10; Length al Similarity 52.5%; Pred. No. 5e-104; 372; Conservative 83; Mismatches 167; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NCV-1999 (TrEMBLrel. 12, Created)
01-NCV-1999 (TrEMBLrel. 12, Last sequence update)
01-NCV-1999 (TrEMBLrel. 20, Last sequence update)
Similar to somatic embryogenesis receptor-like kinase.
F13F21.28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           699 AA; 74329 MW; 97564B8A6389B0BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       DSSQYNEDMKKFRKMALGTQEY---NATGEYSNPTSDYG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTSYNADMKKFRQIALSSQEFPVSDCEGTSSNDSRDMG 625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---SSRSTPSAPPPSPPTPSTPGSPPPLPQPSPPAPT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        699 AA.
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InterPro; IPR002965; P. Lich_extensn.
InterPro; IPR00290; Ser_thr_pkinase.
InterPro; IPR004040; STY_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PR0101; PRCHEXTENSN.
ProDom; PD000001; PINC, 1.
SWART; SW00221; STYEC; 1.
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Matches 372; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
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                                                                                                    SIKALINE-20083487: PubMed-10617187;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.B., Feldblyum T.V.,
Buell C.R., Katchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M. VanAen S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SAPPINSTSSPSPSNTNSTISSP---PAPSPFSPPPQGDSSSSPPPDSTSPPAFQAPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    166 RDEEDAYTVPPPPPPPPPRAGGP---YGGQQQQWRQQNATPPSDHVVTSLPPPPKAPSPPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAPSPGTGSPPSPSNSTTTTPPPASAPPTTFSSPPPSSTIPTSPPPSSRSTPSAPPPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV. COLUMBIA;
Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Lan X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman W.C.,
Fraser C.M., Venter J.C.,
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELOWGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
Hypothetical protein; ATP-binding; Serine/threonine-protein kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 633;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               633 AA; 66651 MW; AE92060E5493C846 CRC64;

    Brassicales; Brassicaceae; Arabidopsis.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; ACOUGLS; AAD12219.1; ...
EMBL; ACOUG439; AAM15257.1; ...
InterPro; IPR000719; Euk_Ekinase.
InterPro; IPR002965; P_rich_extens.
InterPro; IPR002905; Ser_thr_pkinase.
InterPro; IPR004040; Str_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam: PF00069; pkinase; T. PRINTS; PR01217; PR10ERTENSN. Probom; PD000001; Euk_pkinase; 1. SMART; SM00221; STYKC; 1.
                                                                                                                                                                                                                                                                                                                                                Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000)
                                                             FROM N.A.
V. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-CV. COLUMBIA;
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                                                                                                                                                                         Query Match
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Q9LS95;
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Watches
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                    GSPPAPVTPPTRNPPPSVPGPPSNPSREGGSPRPPSSPSSPSPSSDGLSTGVVVGIAIGG 146
                                                                                                                                                                                            EVAVKOLKVGSGQGEREFÇAEVEIISRVHHRHLVSLVGYCI-AGAKRLLVYEFVPNNNLE 357
                                                                                                                                                                                                                                                                                 FGLAKIASDINIHVSIRVMGTFGYLAPEYAASGKLIEKSDVFSFGVVILELIIGRRPVDA 477
ENSSDGSSSSSPPPPSDSSSQSQSPPP-PSTSPPQQSDNNGNKGNNNENNKGNDGSSGDG 127
                                                                        NNVYVDDSLVDWARPLINRASEQGDFEGLADAKMNNGYDREEMARWVACAAACVRHSARR
                                                                                                                                                                                                                                                                                                                                         SG-DMEDSLVDWARPLCMRVAQDGEYGELVDPFLEHQYEPYEMARMVACAAAAVRHSGRR
                                                                                                                                                                                                                                                                                                                                                                                  244 NDHIV-NJAPPPESMGINWVSSPPPPPGNWQPMPSPPARY---SGGANVIQSGEMSSNF
                                                                                                                                                                                                                                       LHLHGEGRPTMEWSTRLK!ALGSAKGLSYLHEDCNPKIIHRDIKASNILIDFKFEAKVAD
                                                                                                                                                                                                                                                                                                                                                                       RPRMSQIVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKKFRKMALGT
                                   VALLVIVILICII.C----KKKRRRDEEDAYYVPPPPPPPPPRAGGPYGGQQQQWRQQNATPP
                                                                                                                                                  SD---RPVLPPPSPGLVLGFSKSTFTYEELARAINGFSEANLLGQGGFGYVHKGVLPSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Terryn N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.,
De Kryser A., Neyt P., Rouze P., Van Den Daele H., Villaroel R.,
Gielen J., van Montagu M., Hoheisel J., Jesse T., Heijnen L., Vos F.
Newes H.W., Mayer K.F.X, Schueller C., Bevan M.;
Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A.

JELYDN N., Ardiles W., Buysshaert C., Dasseville R., De Clerck R.,
Terryn N., Ardiles W., Rouze P., Van Den Daele H., Villaroel R.,
Gielen J., Van Montagu M., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                              QEYNATGEYSNPTSDYGLYPSGSSSEGQTTREMEMG----KIKRTGQG 641
                                                                                                         SDHVVISLPPPP----KAPSPPR----QPPPPPPEMSSSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1998 (TrEMBLrel. 07, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Putative serine/threonine protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            674 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VDSSPAPET-SNGTPPSNGTS---PSNESSPPTPPSSPPPSS---ISAPPDDISASFSPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 PPP-----SGGSPRPPSSPSPBSDGLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 GYVVGIAIGGVALLVIVILICLLCKKKRRRDEEDA----YYVPPPPPPGPKA-GGPYGGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192 QQQWRQQNATPPSDHVVTSLPPPPKAPSPPRQPPPPPPPPFWSSSGGSDYSDRPVLPPPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 YVDDSLVDWARPLLINRASEQGDFEGLADAKMINGYDREEMARWVACAAACVRHSARRPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (MAR-2000) to the EMBL/GeoBank/DDBJ databases.
-!-SIMLARITY: BELOWGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
REMBL; AL023C94; CAA18823.1; -.
REMBL; AL021C94; CAA880161.1; -.
REMBL; AL021C94; CAB80161.1; -.
RICETPO; IPRO0279; EUK_pkinase.
RICETPO; IPRO0409; SEL_thr_pkinase.
R PRODON; PRO00001; SEL_kpkinase.
R PRODON; PRO00001; EUK_pkinase; 1.
SMART; SMO0221; STIKC; 1.
RR PROSITE; PSC0107; PROTEIN_KINASE_ATP; 1.
RR PROSITE; PSC0107; PROTEIN_KINASE_ATP; 1.
RR PROSITE; PSC0101; PROTEIN_KINASE; PROTEIN_KINASE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSSAPSPGTGSPPSSPSNSTTTTPPPASAPPTTPSSPPPSTIPTSPPSSRSTPSAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSPPT----PSTPGSPPPL----PSPPAP--TTPGSPPA-PVTP----PTRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGLVLGFSKSTFTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GEREFGAEVELISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              372 TRLKIALGSAKGLSYLHEDC-----NPKIIHRDIKASNILIDFKFEAKVADFGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MSQ------IVRALEGNVSLSDLNEGMRPGQSNVYSSYGGSTDYDSSQYNEDMKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S---GL------LLLLAVCICICCORRKKKKSPQVNHMHYYKNNNPYGGAPSGNGGYKG-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48.9%; Score 1687; DB 10;
llarity 51.8%; Pred. No. 2.5e-101;
Conservative 87; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 368; Conserv
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342 AKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIK
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InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002965; P_rich_extensn.
InterPro; IPR002290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; Pubmed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REMEMGKIKRIG 639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---SPPSPQGWWNDGNNGNNNDNNNNNNGNWWDAWWGNNKDNNNGNNNGNNNGW 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----TPPTRNPPSVPGPSNPSREGGSPRPPSSPSPSSSD 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GL-----SIGWYWGIAIGGVALLVIVTLICLLCKKKRRRDEEDAYYVPPPPPPGPKA 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPPFMSSSGGSDYSDR-----PVLPPPSPGLVEGFSKSTFTYEELARATNGFSEANLL 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 GSNSSGNNEPNTAAIVGIVAGAGLLFLVMILFCVCCCRKKKKHQMPYY-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----VTSLPPPRAPSPPRQPPPP
                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPASAPPPTTPSSPPPSTIPTSPPSSRSTPSAPPSSPPTPSTPGSPPLPQPSPPAPT
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DNA Res. 7:131-135(2000).

E HELL, ABO26564; BEBO168 JO THE SER/IHR FAMILY OF PROTEIN KINASES. REBL; ABO26564; BEBO1809.1; -.

RICHEPRO, IPR00199: 1, -.

RICHEPRO; IPR002965; P_Lich_extensn.

RICHEPRO; IPR002965; P_Lich_extensn.

RICHEPRO; IPR002965; P_Lich_extensn.

RICHEPRO; IPR002960; Ser_thr_pkinase.

RICHEPRO; IPR004040; STY_pkinase.

REAN; PR01582; KV33CRANNEL.

PRINTS; PR01582; KV33CRANNEL.

PRINTS; PR01217; PRTCHEXTENSN.

PRINTS; PR01217; PRTCHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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PROSITE; PS00107; PROTEIN_KINASE_AIP; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Receptor; Serine/threonine-protein Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10; Length 714;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tch 48.0%; Score 1656.5; D3 10; Length 714; al Similarity 48.2%; Pred. No. 2.6e-99; 353; Conservative 80; Mismatches 146; Indels 153;
                                                                                                                                                                                                                                                                                                                                             Tabata
                                                                                                                                                                                                                                                                                                                                       Kaneko T., Kato T., Asamizu E., Teto the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      947338D8A8B4B250 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Somatic embryogenesis receptor kinase-like protein.
Arabidopsis thallana (Mouse-ear cress).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-COLUMBIA;
MEDLINE-20277480; PubMed-10819329;
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                                                                                                                                                                                                                                                                                                    STRAIN-COLUMBIA;
Sato S., Nakamura Y.,
Submitted (APR-1999) t
                                                                                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Transferase
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RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA Theologis A., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Bushier E., Chan L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Chung M.K., Cond L., Conway A.B., Conway A.B., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldhyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Johnson-Ropon C., Khan S., Khaykin E.,
R. Xim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
R. Langin-Hooper S., Lee A., Lee J.M., Leaz C.R., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
R. Milischer J., Miranda M., Nguyen M., Neoney I., Rowley D.,
RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
Authory M. W. G., Fraser C.M., Vaysorskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Vaysorskaia V.S., Walker M.,
Ra Sequence and analysis of Chromosome I of the plant Arabidopsis
                                                                                                                                507
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                                                                                                                                                                                                                                                                                                                          969
                                                                                                                                                                                                                                                                                402 ASNILIDFKFEAKVADFGLAKIASDINTHVSTRVMGTFG------YLAPEYAASGKL
                                                                          453 TEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDW-----ARPLENRASEQGDFESLA
                                                                                                                                                  DAKMNNGYDREEMARMVACAAACVRHSARRRPRMSQIVRALEGNVSLSDLNBGMRPGQSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids II: Brassicales; Brassicaceae; Arabidopsis.

NCBL_TAXID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TIEMBIREL. 17, Created)
01-JUN-2001 (TIEMBIREL. 17, Last sequence update)
01-JUN-2002 (TIEMBIREL. 21, Last annotation update)
Hypothetical 75.4 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  710 AA.
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Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00220; S_TKC; 1.
SMART; SM00219; TYRC; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
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446
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                                                                                                                                                                                                                                                                                                                                           KRRRDE--BDAYTVPPP-------PPPGPKAGGPTGGQQQWRQQNATPPSDE 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     464
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                                                                                                                                                                                                                                  PP--LPQP-----PPPSV 104
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                                                                                                                         ** SAPPPTTPSSPPPSTI 44
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|SAAPPTDSAPPPSEPADS---SPPPALPSLPPAVFSPPPTVSSPPPPPDL
                                                                                                                                                                                             --STPGSP
                                                                                                                                                                                                                                                          142 PPEQLPPPASSPQGGPKKPKKHHPGPATSPPAPSAPATSPPAPPNAPPRNSSHALPPKST
                                                                                                                                                                                                                                                                                                       202 AAGGPLTSPSR--GVPSSGNSVPPPANSGGGYQGKTMAGERIAGFAVAGAVFLVRRK
                                                                                                                                                                                                                                                                                                                                                          VVTSLPPPPKAPSPPROPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYE
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01-027-2000 (TrEMBLrel. 15, Created)
01-027-2000 (TrEMBLrel. 15, Last sequence update)
01-037-2002 (TrEMBLrel. 20, Last annotation update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Protein kinase-like protein.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptopiyta; Embryophyta; Tracheophyta;
Spermatopixyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
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                                                                                                Gaps
                                                                   DB 10; Length 710;
                                                                                              Indels 149;
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00106; PROTEIN_KINASE_ST; 1.
ATP-binding; Hypothetical protein; Transferase.
SEQUENCE 710 AA; 75371 MW; 8B4420A8DD8F3AA6 CRC64;
                                                                                                                                                                               -----SppTp
                                                                                              158;
                                                                                  Pred. No. 3.6e-90;
81; Mismatches 158
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                                                                   43.9%; Score 1515.5; 46.2%; Pred. No. 3.6e
                                                                                                                        2 SSAPSP-GTGSPPSPSNSTTTTPPPA----
                                                                                                                                                                            45 PTSPPPSSRSTPSAPPP-
                                                                                             Conservative
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                                                                               Similarity
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Best Local Si
Matches 333,
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98 RNPPPSVPGPPSNPSREGGSPRPPS----SPSPPSPSDGLSTGVVVGIAIGGVALLVI 152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEKSDVFSFGVVLLELITGRRPVDANNVYVDDSLVDWARPLLKRASEQGDFEGLADAKMN 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              213 PPPKAPSPPRQPPPPPPPPFMSSSGGSDYSDRPVLPPPSPGLVLGFSKSTFTYEELARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 AP-----IGLVLGIHOSTETYGELARAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLVGYCIAGARRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCN
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                                                                                                                                                           3. II.
3 by ninety
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SMART; SH00201; ENK_pkinase; 1.
SMART; SH00221; STRC; 1.
PROSITE; PS00107; PROTEIN_KINASE_AIP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM: 1.
PROSITE; PS00109; PROTEIN_KINASE_ST; 1.
ATP-binding; Kinase; Serine-threonine-protein kinase; Transferase.
SEQUENCE 567 AA; 63160 MW; ECB5F6DE26855387 CRC64;
                                                                                                                                                                                TAC and BAC clones.*;

DNA Res. 7:217-221(2000).

- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

EMBL; AB020746; BAB02005.1;

InterPro; IPR002199; Buk_pkinase.

InterPro; IPR002190; Ser_thr_pkinase.
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                                                                                                                                                                                                                                                                                                                                                                                                                              93;
                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                            Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3
Sequence features of the regions of 4,251,695 bp covered
                                                                                                                                                                                                                                                                                                                                                                                                  43.8%; Score 1513.5; DB 10; Lengt
64.9%; Pred. No. 3.5e-90;
.ive 37; Mismatches 38; Indels
                                                                o S., Nakamura Y., Asamizu E., Te
the EMBL/GenBank/DDBJ databases
 II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-COLUMBIA;
MEDLINE-20363099; PubMed-10907853;
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                                                                                                                                                                                                                                                                                                                                                                                                                             311; Conservative
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                                                              Kaneko T., Kato T.,
Submitted (DEC-1998)
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 311; Conserv
                                  SEQUENCE FROM N.A.
                                                   STRAIN "COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        095X31;
01-MAY-2000 (
01-MAY-2000 (
                                                                                                      SEQUENCE
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245 ELLVPGSNNPSQNNPTLRPPLDAPNSTNNSGIGTGAVVGISVAVALVVFTLFGIFVWCLR 304
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                                                                                                                                                                                                                                                         323 ISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAK 382
                                                                                                                                                                                                                                                                                                                                           383 GLSYLHEDCNPKIIHRDIKASNILIDFKFFRAKVADFGLAKIASDTNTHVSTRVMGTFGYL 442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           305 KREKRLSAVSGDVTPSPMSSTARSDSAFFRMQSSAPVGASKRSGSFQSGSGGLGNSKAL 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyajima N., Tabata S., "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence features of the 1.6 Mb regions covered by twenty physically assigned
                                                                                                                                                                                                                                                                                                                                                                                                                                APEYAASGKLTEKSDVFSFGVYLLELLTGRRPVDANNYYVDDSLVDWARPLLNRASEQGD
                                                                                                                                                                                                                                                                                                                                                                  Olymar-2001 (Trembirel. 16, Created)
01-Mar-2001 (Trembirel. 16, Last sequence update)
01-Mar-2002 (Trembirel. 21, Last annotation update)
Similarity to protein kinase (Arf918560/MBB18_10).
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids_II: Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                         263 FTYEELARATNGFSEANLLGQGGFGYVHKGVLPSGKEVAVKQLKVGSGQGEREFQAEVEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser I., Carninci P., Dale J.K., Goldsmith A.D., Hayashizari Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S., Arabidopsis CDNA clones.";
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Shinn P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,
Shinn P., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 PGQSNVYSSYGGSTDYDSSQYNEDMKKFRKMALGIQEYN 601
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                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brasslcales; Brasslcaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MSSAP-----SPGIGSPPSPPSNSTT-TTPPPASAP-PPTTP---SSPPPPSIIPTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 PPSSRSTP-----SAPPPSPPTPSTPGSPPPLPQP-----SPP--APTTP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 --SPPSPSSDGLSTGVVVGIAIGGVALLVIVTLICLLCKKKKRRDEEDAYYVPPPPPPGP
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H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 GSPPAP--VTPP-----TRNPPPSV-----PGPPSN-PSREGGSPRPPSSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183 KAGGPYGGXXQQWRQQNATPPSDHVVTSLPPPPK--APSPPRQPPPPPPPFMS-----
                                                                                                                                                                                                                        STRAIN-CV. COLUMBEA,
Vysotskala V.S. Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J.M., Li J., Gonzalez A., Liu R., Takeberg M., Sakano E.,
Chin C., Choi E., Chiou J., Altafi H., Araujo R., Brooks S.,
Buehler E., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
Howng B., Hanizar L., Khan S., Xim C., Rowley D., Shinn P.,
Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
"The sequence of BAC F2435 from Arabidopsis thaliana chromosome l.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.3%; Score 1459.5; DB 10; Length 708;
41.8%; Pred. No. 1.5e-86;
ive 90; Mismatches 127; Indels 225; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATP-binding; Hypothetical protein; Serine/threonine-protein Kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      708 AA; 75127 MW; AC0818E54B076328 CRC64;
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
F2447.8 protein (Hypothetical 75.1 kDa protein).
F2445.8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PP00069; pkinase: 1.
PRINTS; PR01217; PRICHEXTENSN.
Probom: PD000001; Euk_pkinase; 1.
SWART: SM00221; STYKC; 1.
PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_DOM; 1.
PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 ----SSGGSDYSDRPVLPPP------
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Best Local Similarity 41.8*
Matches 317; Conservative
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Query Match
Best Local Similarity 45.99
Matches 313; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSSAPSFGTGSPPSPSRSTTTTPPPASAPPPTTPSSPPPPSTTPTSPPPSSRSTPSAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           186 GPYGGGQQQWRQQNATPPSDHVVTSLPPPFKAPSPPRQPPPPPPPPFMSSSGGSDYSDRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 KVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCIAGAKRLLVYEFVPNNNLELHLHGEGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PTMEWSTRLKIALGSAKGLSYLHEDCNPKIIHRDIKASNILIDEKFEAKVADFGLAKIAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K., Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581;
                                                                                               Sibniticed (JAN-2023) to the EMBL/GenBank/EDBJ databases.

R MSL; AB005231; BAB10146.1; --

R EMSL; AR07681; AALT/6881.; --

R EMSL; AR07681; AALT/6881.; --

R InterPro; IPR000719; Buk_pkinase.

R InterPro; IPR000382; Pistil_extensin.

R InterPro; IPR002896; Pistil_extensin.

R InterPro; IPR002896; Pistil_extensin.

R InterPro; IPR002896; Pistil_extensin.

R InterPro; IPR004346; Tyr_pkinase.

R InterPro; IPR004346; Tyr_pkinase.

R PRINTS; PR01217; PRICHEXTENSIN.

R PRINTS; PR01217; PRICHEXTENSIN.

R PRINTS; PR01218; PSTIEXTENSIN.

R PRINTS; RN00221; STRK; 1.

R SMART; SM00221; STRK; 1.

R SMART; SM00229; Tyrk; 1.

R SMART; SM00229; Tyrk; 1.
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PROSITE; PSO0101; PROTEIN KINASE_DOM; 1.
PROSITE; PSO0108; PROTEIN KINASE_ST; 1.
AIP-Dinding; Kinase; Transferase.
SEQUENCE 681 AA; 72389 MW; F64DAA1E470E73F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42.2%; Score 1456; DB 10;
46.4%; Pred. No. 2.5e-86;
iive 87; Mismatches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Arabidopsis cDNA clones.";
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                                                               Ecker J.R.;
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RA MEDINE-21016719; PubMed-11130712;

RA THOLOGIS A., ECKET J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA Thologis A., Core J.R., Palm C.J., Federspiel N.A., Kaul S.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White D., Connay A.B., Connay A.R., Creasy T.H., Dewar K.,

RA Ching M.K., Conn L., Connay A.B., Connay A.R., Creasy T.H., Dewar K.,

RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

RA Gill J.E., Goldsmith A.D., Haas B., Ransen M.F., Huizar L.,

RA Hunter J.L., Creanentskaia I., Kurtz D.B., Kan B., Langin Hooper S., Lee A., Lee J.M., Leaz C.A., Li J.H., Li Y.-P.,

RA Langin Hooper S., Lee A., Lee J.M., Leaz C.A., Li J.H., Li Y.-P.,

RA Langin Hooper S., Lee A., Luros J.S., Malti R., Marziali A.,

RA Miltscher J., Miranda M., Nayen M., Nachama W.C., Osborne B.I.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

RA Wu B., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

RA Federson and analysis of chromosome I of the plant Arabidopsis
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicacee; Marabidopsis.
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760 AA; 80713 MW; 758EEFIF37C742D7 CRC64;
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45.9%; Pred. No. 7.6e-85;
Mismatches 142;
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PROSITE; PS50011; PROTEIN KINASE DOM; 1.
PROSITE; PS00108; PROTEIN KINASE ST; 1.
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EMBL: AC079829, AA650687.1; -
InterPro: IPR00219; Bul_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR002290; Ser_thr_pkinase.
InterPro: IPR002145; Tyr_pkinase.
Pfam; PF00069; pkinase; 1.
PRINTS: PR01217; PRICHEWTENSN.
PRODOM: PD00001; Buk_pkinase; 1.
SMART: SM00220; S_TKC; 1.
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                                                                                                            LLGQSGFGYVEKGYLPSGKEVAVKQLKVGSGQGEREFQAEVEIISRVHHRHLVSLVGYCI 339
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                                                                                                                                                                                                                                                                                     AGAKRILVYEFVPNNNLELHLHGEGRPTMEWSTRLKIALGSAKGLSYLHEDCNPKITHRD 399
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Vysotskala V.S., Schwartz J.R., Yu G., Toriumi M., Liu S., Lenz C.,
Li J., Kremenetskala I., Luros J., Altafi H., Gonzalez A., Araujo R.,
Buehler E., Conn L., Conway A.B., Dunn P., Hansen N., Buizar L.,
Kim C., Palm C.J., Rowley D., Shinn P., Kalker M., Davis R.W.,
Ecker J.R., Federspiel N.A., Theologis A.;
**Arabidopsis thaliana chromosome 1 BAC F508 sequence.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                        Gaps
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                                                Transferase
PROSITE; PS00107; PROTEIN KINASE_ATP; 1.
PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
ATP-binding; Seriacy-furconine-protein kinase; Transfers SEQUENCE 731 AA; 77639 MW; 45D93AD5C450001B CRC64;
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